

195815

From: Ramirez, Delia  
Sent: Monday, July 17, 2006 11:19 PM  
To: STIC-Biotech/ChemLib  
Subject: 10/716470

Hi,

I would like to request the following search: SEQ ID NO:10 in the protein databases (commercial & interference).

Thank you very much,

Delia M. Ramirez, Ph.D.  
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Recombinant Enzymes-Art Unit 1652  
USPTO  
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delia.ramirez@uspto.gov

CRFE

78701

\*\*\*\*\*  
Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA#: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.9
OM protein - protein search, using sw model	
Run on:	July 19, 2006, 00:21:48 ; Search time 202 Seconds (without alignments) 280.668 Million cell updates/sec
Title:	US-10-716-470-10
Perfect score:	620
Sequence:	1 MVVMEIFITGLLGLASLIS..... BEEPEPTVPPDTPLGVFGGGH 124
Scoring table:	BLASTm62
Searched:	Gapext 0.5
Total number of hits satisfying chosen parameters:	2589679
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	A_Geneseq_8:*
1:	geneseq1990s:*
2:	geneseq1990s:*
3:	geneseq2000s:*
4:	geneseq2001s:*
5:	geneseq2002s:*
6:	geneseq2003as:*
7:	geneseq2003bs:*
8:	geneseq2004s:*
9:	geneseq2005s:*
10:	geneseq2006s:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
Result No.	Query Score Match Length DB ID Description
1	620 100.0 124 6 ABR58214 Abr58214 LysB24 pr
2	620 100.0 124 8 ADO33791 ADO33791 Corynebac
3	620 100.0 124 8 ADO27294 ADO27294 Mutant Co
4	620 100.0 124 8 ADR89160 ADR89160 Amino aci
5	584 94.2 236 2 AAV37715 AAV37715 C. glutamicum
6	584 94.2 236 4 AAG93201 AAG93201 C. glutami
7	584 94.2 236 6 ABR58213 ABR58213 LysB prot
8	584 94.2 236 8 ADO33789 ADO33789 Corynebac
9	584 94.2 236 8 ADO33985 ADO33985 Corynebac
10	584 94.2 236 8 ADO27292 ADO27292 Corynebac
11	584 94.2 236 8 ADR19717 ADR19717 LysB amin
12	579 93.4 236 8 ADR89158 ADR89158 Amino aci
13	576 92.9 236 8 ADO33908 ADO33908 Corynebac
14	571 92.1 233 4 ADR79660 ADR79660 Corynebac
15	571 92.1 233 4 ADR17188 ADR17188 C. glutam
16	571 92.1 233 7 ADR66197 ADR66197 Protein e
17	389.5 62.8 231 4 ADR64749 ADR64749 Corynebac
18	34.4 34.4 211 9 ADR07795 ADR07795 Escherich
19	34.4 34.4 211 9 ADR5027 ADR5027 Escherich
20	34.4 34.4 211 9 ADR89207 ADR89207 Escherich
21	33.1 33.1 213 7 ADR65328 ADR65328 Klebsiell
22	33.1 33.1 213 7 ADR04687 ADR04687 Bacterial
23	29.8 29.8 214 7 ADR04687 ADR04687 Bacterial
ALIGNMENTS	
RESULT 1	
ID	ABR58214 standard; protein: 124 AA.
XX	ABR58214;
XX	AC
DT	23-OCT-2003 (revised)
XX	11-AUG-2003 (First entry)
XX	DE LysE24 protein.
XX	KW L-lysine; L-arginine; LysB24.
OS	Corynebacterium glutamicum.
XX	PN EP1266966-A2.
XX	PD 18-DEC-2002.
XX	PR 05-JUN-2002; 2002EP-00012539.
XX	PR 12-JUN-2001; 2001JP-00177075.
PA	(AJIN ) AJINOMOTO CO INC.
XX	PT Gunji, Y., Yasueda, H;
XX	DR WPI: 2003-24171/24.
XX	N-PSDB; ACC80942.
PS	Claim 8; Page 20, 23pp; English.
XX	The present invention relates to DNA encoding variants of protein with PT when introduced into methanol assimilating bacterium, facilitates PT excretion of L-lysine and/or L-arginine to outside of a cell.
CC	bacterium when introduced into the bacterium. The method is used for CC encoding a protein which facilitates excretion of L-lysine, L-arginine or CC both of these L-amino acids to outside of a cell or a methanol assimilating CC bacterium when DNA of the method is introduced into the bacterium. The present sequence represents a LysB24 protein from CC Brevibacterium lactofermentum. (Updated on 23-OCT-2003 to standardise OS field)

SEQ	Sequence 124 AA;
Query Match	100.0%; Score 620; DB 8; Length 124;
Best Local Similarity	100.0%; Pred. No. 2.9e-68;
Matches	124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MVIMIMIFITGLLGSSLISLISIGPONVLVKGKIREGLIAVLLVLLISDPLFLIGTLGV 60
DB	1 MVIMIMIFITGLLGSSLISLISIGPONVLVKGKIREGLIAVLLVLLISDPLFLIGTLGV 60
QY	61 DLLSNAAPIVLDIINMGGIAYLIPFAMKADMMNKVERQIETEPVPPDPLGV 120
DB	61 DLLSNAAPIVLDIINMGGIAYLIPFAMKADMMNKVERQIETEPVPPDPLGV 120
QY	121 GGGH 124
DB	121 GGGH 124
RESULT 3	
ADO27294	100.0%; Score 620; DB 8; Length 124;
ID	ADO27294 standard; protein; 124 AA.
AC	XX
XX	DT 12-AUG-2004 (first entry)
DE	Mutant Corynebacterium glutamicum truncated LySE protein SeqID 10.
XX	Entner-Dourdorff pathway; methanol metabolism;
KW	6-Phosphogluconate dehydratase; EDD; 2-keto-3-deoxy-6-phosphogluconate aldolase; EDA; L-amino acid; agriculture; food industry; LySE; mutant; mutein.
XX	OS Corynebacterium glutamicum.
OS	Synthetic.
XX	PN FR2847265-A1.
XX	PD 21-MAY-2004.
XX	PF 20-NOV-2003; 2003FR-00013576.
PR	20-NOV-2002; 2002JP-00336346.
XX	(AJIN ) AJINOMOTO CO INC.
PA	Gunji Y, Yasueda H;
PI	XX
DR	WPI; 2004-403038/38.
DR	N-PSDB; ADO27293.
XX	Microbial production of amino acids, useful in agriculture and foods, comprises growing bacteria that use the Entner-Dourdorff pathway for methanol metabolism and have increased activity of enzymes in this pathway.
XX	Disclosure; SEQ ID NO 10; 51pp; French.
PS	This invention relates to the novel production of L-amino acids from microorganisms that use the Entner-Dourdorff pathway for methanol metabolism, such that L-residues are secreted into and recovered from the culture medium. Specifically, it refers to an increase in the activity of two enzymes, namely 6-phosphogluconate dehydratase (EDD) and/ or 2-keto-3-deoxy-6-phosphogluconate aldolase (EDA) that improve production of certain amino acids from an inexpensive carbon source. The present invention describes the production of L-amino acids from a biosynthetic pathway that uses pyruvic acid as an intermediate. Accordingly, this method can be used to produce lysine, leucine, isoleucine and valine, which are amino acids applicable to the agricultural and food industries. This polypeptide sequence is the mutant Corynebacterium glutamicum LySE protein containing an in frame stop codon that truncates the protein prematurely, giving an exemplification of the invention.

XX  
SQ Sequence 124 AA;  
Query Match 100.0%; Score 620; DB 8; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.9e-68;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 MVIMEIFITGLLIGASLLSIGPQNVVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60  
QY 1 MVIMEIFITGLLIGASLLSIGPQNVVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60  
Db 1 MVIMEIFITGLLIGASLLSIGPQNVVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60  
QY 61 DLISNAAPIVLDIMRWGGIAYLILWFAVMAAKDAMTNKVEAQPQIETEPTVPPDTPLGVF 120  
Db 61 DLISNAAPIVLDIMRWGGIAYLILWFAVMAAKDAMTNKVEAQPQIETEPTVPPDTPLGVF 120  
QY 61 DLISNAAPIVLDIMRWGGIAYLILWFAVMAAKDAMTNKVEAQPQIETEPTVPPDTPLGVF 120  
Db 121 GGCH 124  
QY 121 GGCH 124  
Db 121 GGCH 124

RESULT 4  
ADR89160  
ID ADR89160 standard; protein: 124 AA.  
XX  
AC ADR89160;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Amino acid sequence of a mutant lysE gene fragment.  
XX  
KW lysine decarboxylase; enzyme; ldc gene; lysine; cadaverine; L-lysine;  
XX  
KW lysine production; lysE gene.  
XX  
OS Corynebacterium glutamicum.  
XX  
OS Synthetic.  
XX  
PN FR2851575-A1.  
XX  
PD 27-AUG-2004.  
XX  
PP 25-FEB-2004; 2004FR-00001873.  
XX  
PR 25-FEB-2003; 2003JP-00047185.  
XX  
PA (AJINOMOTO CO INC.  
XX  
PI Hirano S, Yasueda H;  
XX  
WPI; 2004618218/60.  
DR N-PSDB; ADR89159.  
XX  
PT Preparation of L-lysine by growing *Methylomonas* in which the endogenous  
PT lysine decarboxylase gene has been inactivated, also new lysine  
PT decarboxylase and nucleic acid encoding it.  
XX  
PS Example 4; SEQ ID NO 24; 57pp; French.

The specification describes a lysine decarboxylase enzyme of  
XX  
CC Methylophilus methylotrophicus. The lysine decarboxylase gene is designated  
CC ldc gene. The lysine decarboxylase enzyme decomposes L-lysine to  
CC cadaverine. M. methylotrophicus cells in which this gene has been reduced  
CC or eliminated are useful for fermentative production of L-lysine in  
CC methanol-based medi. Inactivation of the enzyme increases the efficiency  
CC of lysine production in *Methylophilus* cells. The present sequence is  
CC encoded by a mutated lysE gene fragment, with a thymine inserted after  
CC guanine 355. This fragment was used to construct a plasmid which was then  
CC used to produce L-lysine in cells containing an interrupted ldc gene.  
XX  
Sequence 124 AA;

Query Match 100.0%; Score 620; DB 8; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.9e-68;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 620; DB 8; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.9e-68;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
SQ Sequence 124 AA;  
Query Match 94.2%; Score 584; DB 2; Length 236;  
Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 MVIMEIFITGLLIGASLLSIGPQNVVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60  
QY 1 MVIMEIFITGLLIGASLLSIGPQNVVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60  
Db 1 MVIMEIFITGLLIGASLLSIGPQNVVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60  
QY 61 DLISNAAPIVLDIMRWGGIAYLILWFAVMAAKDAMTNKVEAQPQIETEPTVPPDTPLGVF 118



PN FR2847262-A1.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PR 20-NOV-2003; 2003FR-00013575.  
 XX  
 PT New DNA encoding mutant form of LySE protein, useful for transformation  
 PT of methanol-utilizing bacteria for production of lysine and arginine,  
 PT also new transformants.  
 XX  
 PI Gunji Y, Yasueda H;  
 XX  
 DR WPI; 2004-403035/38.  
 DR N-PSDB; ADO33898.  
 XX  
 PT Methyllobacillus organism, useful for producing lysine and arginine,  
 PT contains DNA encoding variant form of LySE protein that contains only the  
 PT hydrophobic helices.  
 XX  
 PS Example 1; SEQ ID NO 8; 49pp; French.  
 CC  
 CC The invention relates to a novel bacterium of the genus *Methyllobacillus*  
 CC that contains a DNA encoding a variant of the LySE (lysine export)  
 CC protein and is able to produce L-Lys or L-Arg since  
 CC incorporation of the LySE variant induces secretion of Lys and Arg, thus  
 CC improving productivity. The bacterium can be grown on methanol, an  
 CC inexpensive carbon source. The wild-type LySE protein is lethal to  
 CC methanol-utilising bacteria. The current sequence is that of the  
 CC *Corynebacterium glutamicum* LySE (lysine export) wild-type protein of the  
 CC invention.  
 XX  
 SQ Sequence 236 AA;

Query Match 94.2%; Score 584; DB 8; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MVIMIMIFITGILLGASLISLIGPQNLVVIKOGIKREGGLIAVLVCLISDVPLFINGLGV 60  
 Db 1 MVIMIMIFITGILLGASLISLIGPQNLVVIKOGIKREGGLIAVLVCLISDVPLFINGLGV 60  
 QY 61 DLSNAAPIVLDIMRGGLGIAYLWFAVMAAKADMANTNKVEAPQIBETETVPUDDTPLG 118  
 Db 61 DLSNAAPIVLDIMRGGLGIAYLWFAVMAAKADMANTNKVEAPQIBETETVPUDDTPLG 118

RESULT 9  
 ADO33895  
 ID ADO33895 standard; protein; 236 AA.  
 XX  
 AC ADO33895;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Corynebacterium glutamicum LySE protein SeqID 8.  
 XX  
 KW Enmer-bourdonoff pathway; methanol metabolism;  
 KW 6-phosphogluconate dehydrogenase; EDD; 2-keto-3-deoxy-6-phosphogluconate aldolase; EDA; L-amino acid;  
 KW agriculture; food industry; lyse.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 FR2847265-A1.  
 PN  
 PR 21-MAY-2004.  
 XX  
 PT 20-NOV-2003; 2003FR-00013575.  
 XX  
 PR 20-NOV-2002; 2002JP-00336346.  
 XX  
 PA (AJIN ) AJINOMOTO CO INC.  
 XX  
 PI Gunji Y, Yasueda H;  
 XX  
 DR WPI; 2004-403038/38.  
 DR N-PSDB; ADO27291.  
 XX  
 PT Microbial production of amino acids, useful in agriculture and foods,  
 PT comprises growing bacteria that use the Entner-Doudoroff pathway for  
 methanol metabolism and have increased activity of enzymes in this

CC Disclosure; SEQ ID NO 8; 51pp; French.  
 CC XX  
 CC This invention relates to the novel production of L-amino acids from  
 CC microorganisms that use the Entner-Doudoroff pathway for methanol  
 CC metabolism. Specifically, it refers to an increase in the activity of  
 CC culture medium. Specifically, it refers to an increase in the activity of  
 CC two enzymes, namely 6-phosphogluconate dehydrogenase (EDD) and/ or 2-keto-  
 CC -deoxy-6-phosphogluconate aldolase (EDA) that improve production of  
 CC certain amino acids from an inexpensive carbon source. The present  
 CC invention describes the production of L-amino acids from a biosynthetic  
 CC pathway that uses pyruvic acid as an intermediate. Accordingly, this  
 CC method can be used to produce lysine, leucine, isoleucine and valine,  
 CC which are amino acids applicable to the agricultural and food industries.  
 CC This polypeptide sequence is the Corynebacterium glutamicum lysE protein  
 CC given in an exemplification of the invention.  
 XX SQ Sequence 236 AA;  
 Query Match 94 2%; Score 584; DB 8; Length 236;  
 Best Local Similarity 100.0%; Prcd. No. 1.9e-63; Mismatches 0; Indels 0; Gaps 0  
 Matches 118; Conservative 0; MisMatches 0; Indels 0; Gaps 0  
 QY 1 MVVMEIFITGLLGSLLISIGPQWNLVKGQIKREGGLAVLVLISWPLIAIGMV 60  
 Db 1 MVVMEIFITGLLGSLLISIGPQWNLVKGQIKREGGLAVLVLISWPLIAIGMV 60  
 QY 61 DLJSNAAAPTVDLMMRGGTAYLWPFVAMAKDAMTKVQAPQIETEPTVPPDTPLG 118  
 Db 61 DLJSNAAAPTVDLMMRGGTAYLWPFVAMAKDAMTKVQAPQIETEPTVPPDTPLG 118  
 RESULT 11  
 ADR19717  
 ID ADR19717 standard; protein; 236 AA.  
 XX  
 AC ADR19717;  
 XX DT 21-OCT-2004 (first entry)  
 XX DE l-lysE amino acid sequence, seq id 18.  
 XX  
 KW l-lysine; bacteria; methanol; L-methionine; Methylophilus bacteria; metA  
 KW homoserine O-acetyltransferase; lysE.  
 OS Corynebacterium glutamicum.  
 XX PN FR2850394-A1.  
 XX PD 30-JUL-2004.  
 XX PR 29-JAN-2004; 2004FR-00000816.  
 XX PR 29-JAN-2003; 2003JP-00020513.  
 XX (AJIN ) AJINOMOTO CO INC.  
 XX PA WPI; 2004-663572/55.  
 XX DR N-PSDB; ADR19716.  
 XX PT  
 PT utilizing bacteria auxotrophic for L-methionine, preferably new  
 PT Methylophilus strains.  
 PS Disclosure; SEQ ID NO 18; 43pp; French.  
 XX  
 CC The invention relates to the production of L-lysine (I). The method  
 CC involves culturing bacteria which utilise methanol require L-methionine  
 CC (II) for growth and produce (I) in a medium containing methanol as the  
 main carbon source, then recovering the (I) accumulated in the culture.  
 CC Disclosed are Methylophilus bacteria which require (II) for growth and  
 produce (I). Methylophilus bacteria requiring (II) for growth are  
 XX

Query Match	93.4%	Score 579;	DB 8;	Length 236;
Best Local Similarity	99.2%	Pred. No. 1	9e-62;	
Matches	117;	Conservative	0;	Mismatches 0;
		Indels 0;	Gaps 0;	
QY	1	MVIMEIFITGLLIGASLISLISIGPQNLVVIKOGIKREGGLIAVLLVCLSDVFLFTAGTCV	60	QY
Db	1	MVIMEIFITGLLIGASLISLISIGPQNLVVIKOGIKREGGLIAVLLVCLSDVFLFTAGTCV	60	Db
QY	61	DLSNAPVTLIDMRWGGIAYLLWFAWMAAKDAMTNKVEAPOQIEETEPTVPPDTPLG 118	118	QY
Db	61	DLSNAPVTLIDMRWGGIAYLLWFAWMAAKDAMTNKVEAPOQIEETEPTVPPDTPLG 118	118	Db
RESULT 13				RESULT 14
ADO33908				AAB79660
ID ADO33908	standard;	protein;	236 AA.	AAB79660 standard; protein; 233 AA.
XX				XX
AC ADO33908;				AC AAB79660;
XX				XX
DT				DT
XX				XX
DB				DB
corynebacterium glutamicum LysE (lysine export) mutant G56K protein.				Corynebacterium glutamicum MP protein sequence SEQ ID NO:54.
XX				XX
KW				KW Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
KW				KW
lysE; lysine export; methanol-utilising bacterium; S-(2-aminoethyl)cysteine resistance; arginine export; mutant; murein.				lysE; lysine export; methanol-utilising bacterium; S-(2-aminoethyl)cysteine resistance; arginine export; mutant; murein.
XX				XX
OS				OS
Corynebacterium glutamicum.				Corynebacterium glutamicum.
OS				OS
Synthetic.				Synthetic.
XX				XX
FH				FH
Key		Location/Qualifiers		
FT				FT
FT		/note= "Wild-type Gly substituted by Lys"		FT
XX				XX
PN				PN
FR2847264-A1.				FR2847264-A1.
XX				XX
PD				PD
21-MAY-2004.				21-MAY-2004.
XX				XX
PP				PP
20-NOV-2003; 2003FR-00013574.				20-NOV-2003; 2003FR-00013574.
XX				XX
PR				PR
20-NOV-2002; 2002JP-00336315.				20-NOV-2002; 2002JP-00336315.
XX				XX
PA				PA (AJIN')
(AJIN')				AJINOMOTO CO INC.
XX				XX
PI				PI Gunji Y, Yasueda H;
XX				XX
DR				DR WPI; 2004-403037/38.
XX				XX
PT				PT New DNA encoding mutant form of LysE protein, useful for transformation of methanol-utilizing bacteria for production of lysine and arginine, also new transformants.
PT				PT
PT				PT
PS				PS Claim 3; Page; 52pp; French.
XX				XX
CC				CC The invention relates to a novel DNA that encodes a mutant of the LysE (lysine export) protein of a coryneform bacterium, or its homologue, in which at least Gly5 has been replaced by a different amino acid and where the introduction of the DNA into a methanol-utilising bacterium confers resistance to a lysine analogue such as S-(2-aminoethyl)cysteine. The DNA of the invention may be useful since its introduction induces export of Lys and/or Arg from cells, thus facilitating production of these amino acids from an inexpensive carbon source and increasing their concentration in the extracellular medium. The wild-type LysE sequence is not functional in methanol-utilising bacteria. The current sequence is that of the Corynebacterium glutamicum LysE (lysine export) mutant G56K protein of the invention. The current sequence is not shown within the specification per se but was created by the indexer using information given within claim 3.
CC				CC Given within claim 3.
CC				CC Sequence 236 AA;
SQ				SQ
Query Match	92.9%	Score 576;	DB 8;	Length 236;
Best Local Similarity	99.2%	Pred. No. 1	9e-62;	
Matches	117;	Conservative	0;	Mismatches 1;
		Indels 0;	Gaps 0;	



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OM protein -protein search, using sw model

Run on: July 19, 2006, 00:42:58 ; Search time 188 Seconds  
(without alignments)

305.525 Million cell updates/sec

Title: US-10-716-470-10  
Perfect score: 620  
Sequence: 1 MVIMEIFITGLLIGASLILS.....EEETPTVPPDDTPIGLGVFGGHH 124

Scoring table: BLASTM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

1: /EMC\_Celerra\_SDSS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep: \*  
2: /EMC\_Celerra\_SDSS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep: \*  
3: /EMC\_Celerra\_SDSS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep: \*  
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5: /EMC\_Celerra\_SDSS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	620	100.0	124	4 US-10-716-470-10
2	620	100.0	124	4 US-10-716-473-10
3	620	100.0	124	5 US-10-784-986-24
4	620	100.0	124	5 US-10-164-760-10
5	584	94.2	236	3 US-09-738-626-6355
6	584	94.2	236	4 US-10-166-142-8
7	584	94.2	236	4 US-10-716-473-8
8	584	94.2	235	4 US-10-716-480A-2
9	584	94.2	236	4 US-10-760-283-18
10	584	94.2	236	5 US-10-716-470-8
11	584	94.2	235	5 US-09-746-660A-52
12	571	92.1	233	3 US-10-196-232-25
13	571	92.1	233	4 US-10-858-730-224
14	571	92.1	233	5 US-10-855-822-54
15	571	92.1	233	6 US-11-239-674-52
16	571	92.1	233	6 US-11-239-674-52
17	215	34.7	211	6 US-11-115-286-15
18	213	34.4	211	5 US-10-858-730-237
19	170	27.4	199	5 US-10-858-730-93
20	154	24.8	201	5 US-10-858-730-94
21	149	24.0	204	5 US-10-858-730-95
22	140	22.6	203	4 US-10-156-761-8659
23	104	16.8	212	4 US-10-374-903A-6
24	93	15.0	211	4 US-10-212-2A-47826
25	91	14.7	210	4 US-10-335-977-5883
26	91	14.7	210	4 US-10-335-977-5884
27	215	4	US-10-335-977-5885	

RESULT 1	US-10-166-142-10
;	Sequence 10, Application US/10166142
;	Publication No. US20030124687A1
;	GENERAL INFORMATION:
;	APPLICANT: YASUDA, HISASHI
;	TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL ASSIMILATING BACTERIUM
;	TITLE OF INVENTION: ASSIMILATING BACTERIUM
;	FILE REFERENCE: 223799US
;	CURRENT APPLICATION NUMBER: US10/166,142
;	CURRENT FILING DATE: 2003-06-11
;	PRIOR APPLICATION NUMBER: JP 2001-177707
;	PRIOR FILING DATE: 2001-06-12
;	NUMBER OF SEQ ID NOS: 10
;	SOFTWARE: PatentIn version 3.1
;	SEQ ID NO: 10
;	LENGTH: 124
;	TYPE: PRT
;	ORGANISM: Brevibacterium lactofermentum
;	US-10-166-142-10
;	Query Match Similarity 100.0%; Score 620; DB 4; Length 124;
;	Best Local Similarity 100.0%; Score 620; DB 4; Length 124;
;	Matches 124; Conservative 0; Mismatches 0; Gaps 0; Indels 0;
;	Query 1 MVIMEIFITGLLIGASLILS.....EEETPTVPPDDTPIGLGVFGGHH 60
;	Db 1 MVIMEIFITGLLIGASLILS.....EEETPTVPPDDTPIGLGVFGGHH 60
;	QY 61 DLNSNAPIVLDIWRWGJIAYLWFAVMKAQDANTKVEAPQIETEETPTVPPDDTPIGLGV 120
;	Db 61 DLNSNAPIVLDIWRWGJIAYLWFAVMKAQDANTKVEAPQIETEETPTVPPDDTPIGLGV 120
;	QY 121 GGGH 124
;	Db 121 GGGH 124
;	RESULT 2
;	US-10-716-473-10
;	Sequence 10, Application US/10716473
;	Publication No. US200401243541
;	GENERAL INFORMATION:
;	APPLICANT: Ajinomoto Co. Inc
;	TITLE OF INVENTION: Method For Producing L-Amino Acid Using Methylotroph
;	FILE REFERENCE: OP6129
;	CURRENT APPLICATION NUMBER: US/10/166,142
;	CURRENT FILING DATE: 2003-11-20
;	PRIOR APPLICATION NUMBER: JP 2002-336346

PRIOR FILING DATE: 2002-11-20  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO: 10  
 LENGTH: 124  
 TYPE: PRT  
 ORGANISM: *Brevibacterium lactofermentum*  
 US-10-716-473-10

Query Match 100.0%; Score 620; DB 4; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-63; Mismatches 0; Indels 0; Gaps 0;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVIMEIFITGLLGASLLSISGPNVLVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60  
 Db 1 MVIMEIFITGLLGASLLSISGPNVLVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60

Qy 61 DLSNSNAPIVLDIMRWWGGIAYLWFAVMKAQDAMTNKVEAPQIETEPTVDDTPGVF 120  
 Db 61 DLSNSNAPIVLDIMRWWGGIAYLWFAVMKAQDAMTNKVEAPQIETEPTVDDTPGVF 120

Qy 121 GGGH 124  
 Db 121 GGGH 124

RESULT 3  
 US-10-784-986-24  
 Sequence 24, Application US/10784986  
 Publication No. US2004022931A1  
 GENERAL INFORMATION:  
 APPLICANT: HIRANO, Seiko  
 TITLE OF INVENTION: Novel lysine decarboxylase gene and method for  
 TITLE OF INVENTION: Producing L-lysine  
 FILE REFERENCE: US-109  
 CURRENT APPLICATION NUMBER: US/10/784, 986  
 CURRENT FILING DATE: 2004-02-25  
 PRIOR APPLICATION NUMBER: JP 2003-47185  
 PRIOR FILING DATE: 2003-02-25  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO: 24  
 LENGTH: 124  
 TYPE: PRT  
 ORGANISM: *Brevibacterium lactofermentum*  
 US-10-784-986-24

Query Match 100.0%; Score 620; DB 5; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-63; Mismatches 0; Indels 0; Gaps 0;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVIMEIFITGLLGASLLSISGPNVLVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60  
 Db 1 MVIMEIFITGLLGASLLSISGPNVLVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60

Qy 61 DLSNSNAPIVLDIMRWWGGIAYLWFAVMKAQDAMTNKVEAPQIETEPTVDDTPGVF 120  
 Db 61 DLSNSNAPIVLDIMRWWGGIAYLWFAVMKAQDAMTNKVEAPQIETEPTVDDTPGVF 120

Qy 121 GGGH 124  
 Db 121 GGGH 124

RESULT 4  
 US-10-716-470-10  
 Sequence 10, Application US/10716470  
 Publication No. US20050003495A1  
 GENERAL INFORMATION:  
 APPLICANT: Ajinomoto Co. Inc.  
 TITLE OF INVENTION: Method For Producing L-Lysine or L-Arginine By Using  
 TITLE OF INVENTION: Method For Producing L-Lysine or L-Arginine By Using

Query Match 94.2%; Score 584; DB 3; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-59; Mismatches 0; Indels 0; Gaps 0;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVIMEIFITGLLGASLLSISGPNVLVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60  
 Db 1 MVIMEIFITGLLGASLLSISGPNVLVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60

Qy 61 DLSNSNAPIVLDIMRWWGGIAYLWFAVMKAQDAMTNKVEAPQIETEPTVDDTPGVF 118  
 Db 61 DLSNSNAPIVLDIMRWWGGIAYLWFAVMKAQDAMTNKVEAPQIETEPTVDDTPGVF 118

Qy 121 GGGH 124  
 Db 121 GGGH 124

Query Match 100.0%; Score 620; DB 5; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-63; Mismatches 0; Indels 0; Gaps 0;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVIMEIFITGLLGASLLSISGPNVLVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60  
 Db 1 MVIMEIFITGLLGASLLSISGPNVLVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60

Qy 61 DLSNSNAPIVLDIMRWWGGIAYLWFAVMKAQDAMTNKVEAPQIETEPTVDDTPGVF 120  
 Db 61 DLSNSNAPIVLDIMRWWGGIAYLWFAVMKAQDAMTNKVEAPQIETEPTVDDTPGVF 120

Qy 121 GGGH 124  
 Db 121 GGGH 124

Query Match 100.0%; Score 620; DB 5; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-63; Mismatches 0; Indels 0; Gaps 0;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVIMEIFITGLLGASLLSISGPNVLVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60  
 Db 1 MVIMEIFITGLLGASLLSISGPNVLVIKOGIKREGGLIAVLVCLISDVFLFLAGTV 60

Qy 61 DLSNSNAPIVLDIMRWWGGIAYLWFAVMKAQDAMTNKVEAPQIETEPTVDDTPGVF 118  
 Db 61 DLSNSNAPIVLDIMRWWGGIAYLWFAVMKAQDAMTNKVEAPQIETEPTVDDTPGVF 118

Db 61 DLLSNAAPIVLDIMRWGGIAYLLWFAWMAKDAMTNKVEAPOIETEPTVPPDTPLG 118 ; Sequence 2, Application US/10716480A  
; Publication No. US2004014697A1  
; GENERAL INFORMATION:  
; Publication No. US20030124687A1  
; APPLICANT: GUNJI, YOSHIYA  
; TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACID USING METHYLOTROPH  
; TITLE OF INVENTION: Method for Producing L-Amino Acid Using Methylotroph  
; FILE REFERENCE: 223789US  
; CURRENT APPLICATION NUMBER: US/10/166,142  
; CURRENT FILING DATE: 2002-06-11  
; PRIORITY NUMBER: JP 2001-177075  
; PRIORITY FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 8  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Brevibacterium lactofermentum  
; US-10-166-42-8

Query Match 94.2%; Score 584; DB 4; Length 236;  
Best Local Similarity 100.0%; Pred. No. 6.3e-59; Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MVIMEIFITGLLIGASLLSIGPONVLVKGKREGGLAVULVCLISDVFLIFIAGTLGV 60  
Db 1 MVIMEIFITGLLIGASLLSIGPONVLVKGKREGGLAVULVCLISDVFLIFIAGTLGV 60

RESULT 7  
US-10-716-473-8  
; Sequence 8, Application US/10716473  
; Publication No. US20040142435A1  
; GENERAL INFORMATION:  
; APPLICANT: Ajinomoto Co. Inc.  
; TITLE OF INVENTION: Method for Producing L-Amino Acid Using Methylotroph  
; FILE REFERENCE: OPI629  
; CURRENT APPLICATION NUMBER: US/10/716,473  
; CURRENT FILING DATE: 2003-11-20  
; PRIORITY APPLICATION NUMBER: JP 2002-336346  
; PRIORITY FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Brevibacterium lactofermentum  
; US-10-716-473-8

Query Match 94.2%; Score 584; DB 4; Length 236;  
Best Local Similarity 100.0%; Pred. No. 6.3e-59; Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MVIMEIFITGLLIGASLLSIGPONVLVKGKREGGLAVULVCLISDVFLIFIAGTLGV 60  
Db 1 MVIMEIFITGLLIGASLLSIGPONVLVKGKREGGLAVULVCLISDVFLIFIAGTLGV 60

RESULT 9  
US-10-760-283-18  
; Sequence 18, Application US/10760283  
; Publication No. US20040214296A1  
; GENERAL INFORMATION:  
; APPLICANT: ASAHARA, Takayuki  
; APPLICANT: HIRANO, Seiko  
; APPLICANT: YASUEDA, Hisashi  
; TITLE OF INVENTION: Method for Producing L-Lysine Using Methanol-utilizing Bacterium  
; FILE REFERENCE: OPI631  
; CURRENT APPLICATION NUMBER: US/10/760,283  
; CURRENT FILING DATE: 2004-01-21  
; PRIORITY NUMBER: JP 2003-30513  
; PRIORITY FILING DATE: 2003-01-29  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Brevibacterium lactofermentum  
; US-10-760-283-18

Query Match 94.2%; Score 584; DB 4; Length 236;  
Best Local Similarity 100.0%; Pred. No. 6.3e-59; Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MVIMEIFITGLLIGASLLSIGPONVLVKGKREGGLAVULVCLISDVFLIFIAGTLGV 60  
Db 1 MVIMEIFITGLLIGASLLSIGPONVLVKGKREGGLAVULVCLISDVFLIFIAGTLGV 60

RESULT 10  
US-10-784-986-22  
; Sequence 22, Application US/10784986  
; Publication No. US2004022931A1  
; GENERAL INFORMATION:  
; APPLICANT: HIRANO, Seiko  
; APPLICANT: YASUEDA, Hisashi

RESULT 8  
US-10-716-480A-2

TITLE OF INVENTION: Novel lysine decarboxylase gene and method for  
 TITLE OF INVENTION: producing L-lysine  
 FILE REFERENCE: US-109  
 CURRENT APPLICATION NUMBER: US/10/784, 986  
 CURRENT FILING DATE: 2004-02-25  
 PRIORITY APPLICATION NUMBER: JP 2003-47185  
 PRIORITY FILING DATE: 2003-02-25  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 22  
 LENGTH: 236  
 TYPE: PRT  
 ORGANISM: *Brevibacterium lactofermentum*  
 US-10-784-986-22

Query Match 94.2%; Score 584; DB 5; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-59; Mismatches 0; Indels 0; Gaps 0;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PRIORITY APPLICATION NUMBER: 60/141031  
 PRIORITY FILING DATE: 2000-06-22  
 PRIORITY APPLICATION NUMBER: 09/606740  
 PRIORITY FILING DATE: 2000-06-23  
 PRIORITY APPLICATION NUMBER: 09/603124  
 PRIORITY FILING DATE: 2000-06-23  
 PRIORITY APPLICATION NUMBER: 60/148613  
 PRIORITY FILING DATE: 1999-07-02  
 PRIORITY APPLICATION NUMBER: 60/148613  
 PRIORITY FILING DATE: 1999-08-12  
 PRIORITY APPLICATION NUMBER: 60/187870  
 PRIORITY FILING DATE: 2000-03-09  
 PRIORITY APPLICATION NUMBER: DE 19931420.9  
 PRIORITY FILING DATE: 1999-07-08  
 NUMBER OF SEQ ID NOS: 125  
 SOFTWARE: PatentIn Vers. 2.0  
 SEQ ID NO 52  
 LENGTH: 233  
 TYPE: PRT  
 ORGANISM: *Corynebacterium glutamicum*  
 US-09-746-660A-52

Query Match 94.2%; Score 584; DB 5; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-59; Mismatches 0; Indels 0; Gaps 0;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PRIORITY APPLICATION NUMBER: 60/141031  
 PRIORITY FILING DATE: 2000-06-22  
 PRIORITY APPLICATION NUMBER: 09/606740  
 PRIORITY FILING DATE: 2000-06-23  
 PRIORITY APPLICATION NUMBER: 09/603124  
 PRIORITY FILING DATE: 2000-06-23  
 PRIORITY APPLICATION NUMBER: 60/148613  
 PRIORITY FILING DATE: 1999-07-02  
 PRIORITY APPLICATION NUMBER: 60/148613  
 PRIORITY FILING DATE: 1999-08-12  
 PRIORITY APPLICATION NUMBER: 60/187870  
 PRIORITY FILING DATE: 2000-03-09  
 PRIORITY APPLICATION NUMBER: DE 19931420.9  
 PRIORITY FILING DATE: 1999-07-08  
 NUMBER OF SEQ ID NOS: 125  
 SOFTWARE: PatentIn Vers. 2.0  
 SEQ ID NO 52  
 LENGTH: 233  
 TYPE: PRT  
 ORGANISM: *Corynebacterium glutamicum*  
 US-09-746-660A-52

RESULT 11  
 US-10-716-470-8

Sequence 8, Application US/10/16470  
 Publication No. US2005003495A1  
 GENERAL INFORMATION:  
 APPLICANT: Ajinomoto Co. Inc.  
 TITLE OF INVENTION: Method For Producing L-Lysine or L-Arginine By Using  
 FILE REFERENCE: OP1628  
 CURRENT APPLICATION NUMBER: US/10/716, 470  
 CURRENT FILING DATE: 2003-11-20  
 PRIORITY APPLICATION NUMBER: JP 2002-336340  
 PRIORITY FILING DATE: 2002-11-20  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 8  
 LENGTH: 236  
 TYPE: PRT  
 ORGANISM: *Brevibacterium lactofermentum*  
 US-10-716-470-8

Query Match 94.2%; Score 584; DB 5; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-59; Mismatches 0; Indels 0; Gaps 0;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PRIORITY APPLICATION NUMBER: 60/141031  
 PRIORITY FILING DATE: 2000-06-22  
 PRIORITY APPLICATION NUMBER: 09/606740  
 PRIORITY FILING DATE: 2000-06-23  
 PRIORITY APPLICATION NUMBER: 09/603124  
 PRIORITY FILING DATE: 2000-06-23  
 PRIORITY APPLICATION NUMBER: 60/148613  
 PRIORITY FILING DATE: 1999-07-02  
 PRIORITY APPLICATION NUMBER: 60/148613  
 PRIORITY FILING DATE: 1999-08-12  
 PRIORITY APPLICATION NUMBER: 60/187870  
 PRIORITY FILING DATE: 2000-03-09  
 PRIORITY APPLICATION NUMBER: DE 19931420.9  
 PRIORITY FILING DATE: 1999-07-08  
 NUMBER OF SEQ ID NOS: 125  
 SOFTWARE: PatentIn Vers. 2.0  
 SEQ ID NO 52  
 LENGTH: 233  
 TYPE: PRT  
 ORGANISM: *Corynebacterium glutamicum*  
 US-09-746-660A-52

RESULT 13  
 US-10-196-232-25

Sequence 25, Application US/10/196232  
 Publication No. US2003011389A1  
 GENERAL INFORMATION:  
 APPLICANT: Yamaguchi, Mikiko  
 APPLICANT: Ito, Hisao  
 APPLICANT: Gunji, Yoshiya  
 APPLICANT: Yasuda, Hisashi  
 TITLE OF INVENTION: METHOD FOR PRODUCING L-ARGININE  
 FILE REFERENCE: 225391US0  
 CURRENT APPLICATION NUMBER: US/10/196, 232  
 CURRENT FILING DATE: 2002-07-17  
 PRIORITY APPLICATION NUMBER: JP 2001-224586  
 PRIORITY FILING DATE: 2001-07-25  
 NUMBER OF SEQ ID NOS: 35  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 25  
 LENGTH: 233  
 TYPE: PRT  
 ORGANISM: *Corynebacterium glutamicum*  
 US-10-196-232-25

Query Match 92.1%; Score 571; DB 4; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 2e-57; Mismatches 0; Indels 0; Gaps 0;  
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PRIORITY APPLICATION NUMBER: 60/141031  
 PRIORITY FILING DATE: 2000-06-22  
 PRIORITY APPLICATION NUMBER: 09/606740  
 PRIORITY FILING DATE: 2000-06-23  
 PRIORITY APPLICATION NUMBER: 09/603124  
 PRIORITY FILING DATE: 2000-06-23  
 PRIORITY APPLICATION NUMBER: 60/148613  
 PRIORITY FILING DATE: 1999-07-02  
 PRIORITY APPLICATION NUMBER: 60/148613  
 PRIORITY FILING DATE: 1999-08-12  
 PRIORITY APPLICATION NUMBER: 60/187870  
 PRIORITY FILING DATE: 2000-03-09  
 PRIORITY APPLICATION NUMBER: DE 19931420.9  
 PRIORITY FILING DATE: 1999-07-08  
 NUMBER OF SEQ ID NOS: 125  
 SOFTWARE: PatentIn Vers. 2.0  
 SEQ ID NO 52  
 LENGTH: 233  
 TYPE: PRT  
 ORGANISM: *Corynebacterium glutamicum*  
 US-10-196-232-25

RESULT 12  
 US-09-746-660A-52

Sequence 52, Application US/09/746660A  
 Publication No. US2003049804A1  
 GENERAL INFORMATION:  
 APPLICANT: Pompejus, Markus  
 APPLICANT: Kroger, Burkhard  
 APPLICANT: Schroder, Hartwig  
 APPLICANT: Zelder, Oskar  
 APPLICANT: Haberhauer, Gregor  
 APPLICANT: Kim, Jun-Won

RESULT 14  
 US-10-858-730-234  
 ; Sequence 234, Application US/10058730  
 ; Publication No. US20050255568A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bailey, Richard B.  
 ; APPLICANT: Blomquist, Paul  
 ; APPLICANT: Doten, Reed  
 ; APPLICANT: Driggers, Edward M.  
 ; APPLICANT: Madden, Kevin T.  
 ; APPLICANT: O'Leary, Jessica  
 ; APPLICANT: O'Toole, George  
 ; APPLICANT: Trueheart, Joshua  
 ; APPLICANT: Walbridge, Michael J.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID  
 ; TITLE OF INVENTION: PRODUCTION  
 ; FILE REFERENCE: 1-4184-030001  
 ; CURRENT APPLICATION NUMBER: US/10/858,730  
 ; CURRENT FILING DATE: 2004-06-01  
 ; PRIOR APPLICATION NUMBER: US 60/475,000  
 ; PRIOR FILING DATE: 2003-05-30  
 ; PRIOR APPLICATION NUMBER: US 60/551,860  
 ; PRIOR FILING DATE: 2004-03-10  
 ; NUMBER OF SEQ ID NOS: 364  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 234  
 ; LENGTH: 233  
 ; TYPE: PRT  
 ; ORGANISM: Corynebacterium glutamicum  
 ; US-10-858-730-234

Query Match 92.1%; Score 571; DB 5; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 2e-57; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MEIFITGIGLIGASLLSIGPQNLVVIKOGIKREGGLIAYLVLVCLISDVFLFINGTLGVDLL 63  
 Db 1 MEIFITGIGLIGASLLSIGPQNLVVIKOGIKREGGLIAYLVLVCLISDVFLFAGTLGVDLL 60

QY 64 SNAPYVIDIMWGGIAYLWVMAAKDAMTNKVEAQPQIETEPTVPPDPLG 118  
 Db 61 SNAAPYVIDIMWGGIAYLWVMAAKDAMTNKVEAQPQIETEPTVPPDPLG 115

RESULT 15  
 US-11-055-822-54  
 ; Sequence 54, Application US/11055822  
 ; Publication No. US20050260707A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pompeius, Markus  
 ; APPLICANT: Kroger, Burkhard  
 ; APPLICANT: Schroder, Hartwig  
 ; APPLICANT: Zelder, Oskar  
 ; APPLICANT: Haberhauer, Gregor  
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
 ; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS  
 ; FILE REFERENCE: BGI-121CCN  
 ; CURRENT APPLICATION NUMBER: US/11/055,822  
 ; CURRENT FILING DATE: 2005-02-11  
 ; PRIOR APPLICATION NUMBER: 09/605,740  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: 60/141,031  
 ; PRIOR FILING DATE: 1999-06-25  
 ; PRIOR APPLICATION NUMBER: 60/142,101  
 ; PRIOR FILING DATE: 1999-07-02  
 ; PRIOR APPLICATION NUMBER: 60/148,613  
 ; PRIOR FILING DATE: 1999-08-12

Query Match 92.1%; Score 571; DB 6; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 2e-57; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MEIFITGIGLIGASLLSIGPQNLVVIKOGIKREGGLIAYLVLVCLISDVFLFAGTLGVDLL 63  
 Db 1 MEIFITGIGLIGASLLSIGPQNLVVIKOGIKREGGLIAYLVLVCLISDVFLFAGTLGVDLL 60

QY 64 SNAPYVIDIMWGGIAYLWVMAAKDAMTNKVEAQPQIETEPTVPPDPLG 118  
 Db 61 SNAAPYVIDIMWGGIAYLWVMAAKDAMTNKVEAQPQIETEPTVPPDPLG 115

Search completed: July 19, 2006, 00:46:18  
 Job time : 189 secs

OM protein - protein search, using SW model  
 Run on: July 19, 2006, 00:25:46 ; search time 40 Seconds  
 (without alignments)  
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**Title:** US-10-716-470-10  
**Perfect score:** 620  
**Sequence:** 1 MVIMIEFIFTGLLIGASILS. .... EETEPRTVPPDDTPLGVFGGGH 124  
**Scoring table:** BLOSUM62  
**Gapp:** 10.0 , **Gapext:** 0.5  
**Searched:** 283416 seqs, 96216763 residues  
**Post-processing:** Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries  
**database :**  
 PIR\_80.0:  
 1: pi1:/\*  
 2: pi2:/\*  
 3: pi3:/\*  
 4: pi4:/\*  

**pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Length	Match Length	DB ID	Description
1	213	34.4	211	1 Q0EC5A	hypothetical 23K P
2	210	33.9	211	2 E85948	hypothetical prote
3	210	33.9	211	2 B91103	hypothetical prote
4	205	33.1	211	2 AH0874	probable membrane
5	199.5	32.2	205	2 AG0112	probable LysE type
6	193.5	31.2	202	2 C97472	probable membrane
7	193.5	31.2	202	2 E82690	LysE family transp
8	172.5	27.8	200	2 D83100	probable transport
9	170	27.4	199	2 H70756	probabilistic prote
10	169	27.3	204	2 AD3411	transporter, LysE
11	154	24.8	201	2 C70744	hypothetical prote
12	135.	21.8	211	2 S57940	Ygga protein homol
13	116	18.7	211	2 B82318	LysE/Ygga family P
14	109	17.6	210	2 D84016	hypothetical prote
15	107	17.3	210	2 B87252	hypothetical prote
16	105	16.9	220	2 D69838	hypothetical protein
17	104	16.8	205	2 B88754	conserved hypothet
18	99	16.0	212	2 AD0714	probable membrane
19	94.5	15.2	235	2 AD2904	RhtB family transp
20	94.5	15.2	235	2 F97679	hypothetical prote
21	94	15.2	215	2 AH3203	RhtB family transp
22	92	14.8	200	2 G83703	hypothetical prote
23	91	14.7	208	2 G84086	dihydrodipicolinat
24	91	14.7	210	2 F64609	conserved hypothet
25	91	14.7	210	2 F71906	hypothetical prote
26	88.5	14.3	212	2 F64940	hypothetical prote
27	87	14.0	195	2 AF0810	probable membrane
28	86	13.9	197	2 B83280	hypothetical prote
29	86	13.9	207	2 E83703	hypothetical prote

**SUMMARIES**

## SUMMARIES

## ALIGNMENT:

Nature 409, 529-533, 2001  
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A;Reference number: A85480; MUID:21074935; PMID:11206551  
 A;Accession: B85948  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-211 <STO>  
 A;Cross-references: UNIPROT:Q8XD10; UNIPARC:UPI0000165916; GB:AB005174; NID:gi12517455;  
 A;Experimental source: strain O157:H7, substrain EDL933  
 C;Genetics:  
 A;Gene: ygga  
 C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)  
 Query Match 33.9%; Score 210; DB 2; Length 211;  
 Best local Similarity 35.1%; Pred. No. 1.3e-13; Gaps 3;  
 Matches 47; Conservative 27; Mismatches 42; Indels 18; Gaps 3;  
 Qy 7 FITGILGASLLSIGPONVVLTKOGIKREGGLAVLVLCLISDVFLFLAGTLGVDSL 66  
 Db 5 YFOGLALGAAAMILPLGPONAFVNQNGIRROHIMALLCAISDLVLCAGIFGGSALLMQ 64  
 Qy 67 APIVIDIMRNGGIAVLWFAVMAKDAMTKVE--AQPIEE-----TEPT 110  
 Db 65 SPWLIALVTVGGWVFLWYFGAKTAMSSNIELASEAVKQGRWKIATMLAVLWLNPH 124  
 Qy 111 VPDDT--PLGVFGG 122  
 Db 125 VYLDTFVNLGSLGG 138

RESULT 3  
 B91103  
 C;Species: Escherichia coli [imported] - Escherichia coli (strain O157:H7, substrain RI  
 C;IDate: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
 C;Accession: B91103  
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 Gesswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
 A;Reference number: A99629; MUID:21156231; PMID:11258796  
 A;Accession: B91103  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-211 <HAY>  
 A;Cross-references: UNIPROT:Q8XD10; UNIPARC:UPI00000D03F2; GB:BA000007; PIDN:BAB37217.1;  
 A;Experimental source: strain O157:H7, substrain RIMD 0509952  
 C;Genetics:  
 A;Gene: EC83794  
 C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)  
 Query Match 33.9%; Score 210; DB 2; Length 211;  
 Best local Similarity 35.1%; Pred. No. 1.3e-13; Gaps 3;  
 Matches 47; Conservative 27; Mismatches 42; Indels 18; Gaps 3;  
 Qy 7 FITGILGASLLSIGPONVVLTKOGIKREGGLAVLVLCLISDVFLFLAGTLGVDSL 66  
 Db 5 YFOGLALGAAAMILPLGPONAFVNQNGIRROHIMALLCAISDLVLCAGIFGGSALLMQ 64  
 Qy 67 APIVIDIMRNGGIAVLWFAVMAKDAMTKVE--AQPIEE-----TEPT 110  
 Db 65 SPWLIALVTVGGWVFLWYFGAKTAMSSNIELASEAVKQGRWKIATMLAVLWLNPH 124  
 Qy 111 VPDDT--PLGVFGG 122  
 Db 125 VYLDTFVNLGSLGG 138

RESULT 4  
 AH0874  
 C;Species: Agrobacterium tumefaciens  
 C;IDate: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
 C;Accession: C97472  
 R;Goodner, B.; Hinkle, G.; Gatung, S.; Miller, N.; Blanchard, M.; Quroollo, B.; Goldman, A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 A;Note: this species has also been called *Salmonella* *typhi*

RESULT 5  
 AG0112  
 C;Species: Yersinia pestis  
 C;IDate: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C;Accession: AG0112  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B.; de-ni-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature 413, 523-527, 2001  
 A;Title: Sequence of *Yersinia pestis*, the causative agent of plague.  
 A;Reference number: AB00001; MUID:21470413; PMID:11586360  
 A;Accession: AG0112  
 A;Molecule type: DNA  
 A;Residues: 1-205 <KUR>  
 A;Cross-references: UNIPROT:Q8ZH6; UNIPARC:UPI00000DC792; GB:AL590842; PIDN:CAC89762.1;  
 C;Genetics:  
 A;Gene: YFO0918  
 C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)  
 Query Match 32.2%; Score 199.5; DB 2; Length 205;  
 Best local Similarity 38.5%; Pred. No. 1.4e-12; Gaps 1;  
 Matches 35; Conservative 27; Mismatches 26; Indels 3; Gaps 1;  
 Qy 3 IMETFITGILGASLLSIGPONVVLTKOGIKREGGLAVLVLCLISDVFLFLAGTLGVDSL 62  
 Db 1 MLAVYHFLPISAMILPLGPONAFVNQNGIRROHIMALLCAISDLVLCAGIFGGS 60  
 Qy 63 LSNAPIDLIMRNGGIAVLWFAVMAKDAMTKVE--AVMAA 90  
 Db 61 LLRSRSPWLIALVTVGGWVFLWYFGAKTAMSSNIELASEAVKQGRWKIATMLAVLWLNPH 91

RESULT 6  
 C97472  
 C;Species: Agrobacterium tumefaciens  
 C;IDate: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
 C;Accession: C97472  
 R;Goodner, B.; Hinkle, G.; Gatung, S.; Miller, N.; Blanchard, M.; Quroollo, B.; Goldman, A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;



A;Accession: AD3411  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-204 <KUR>  
 A;Cross-references: UNIPROT:Q8YGB7; UNIPARC:UPI000057FE3; GB:AE008917; PIDN:AAL52455.1;  
 A;Experimental source: strain 16M  
 A;Gene: BMEII1274  
 A;Map position: I  
 C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)

Query Match 27.3%; Score 169; DB 2; Length 204;  
 Best Local Similarity 35.4%; Pred. No. 1.5e-09; Mismatches 36; Indels 2; Gaps 1;  
 Matches 34; Conservative 24; Mismatches 36; Indels 2; Gaps 1;

QY 8 ITGLLIGASILLISIGPQNVVVIKOGIKREGGLIAVILVCLISDVFLPIAGTLGVLDLSNA 67  
 Db 6 LSGERLIGASILIAIGAQNPLRQSLRQFLCILICALSDDALISAGWAGLILAS 65

QY 68 PIVIDLIMRGGIAYIILWFAVMAAKUDATNKVEAPOII 103  
 Db 66 PKLIAFVTLAGAAFLFWIYASVAFRRRF-HPEAMOV 99

RESULT 11  
 C70744 hypothetical protein Rv0488 - Mycobacterium tuberculosis (strain H37RV)  
 C;Species: Mycobacterium tuberculosis  
 C;Accession: C70744  
 C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
 R;Cole, S.T.; Broach, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentle, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squats, S.; Nature 393, 537-544, 1998  
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A;Reference number: A70500; MUID:98295987; PMID:9634230  
 A;Accession: C70744  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-201 <COL>  
 A;Cross-references: UNIPROT:Q11154; UNIPARC:UPI000139897; GB:277162; GB:ALL23456; NID:9  
 A;Experimental source: strain H37RV  
 C;Genetics:  
 A;Gene: Rv0488  
 C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)

Query Match 24.8%; Score 154; DB 2; Length 201;  
 Best Local Similarity 39.7%; Pred. No. 4.6e-08; Mismatches 31; Conservative 23; Mismatches 24; Indels 0; Gaps 0;

QY 16 SLSISIGPQNVVVIKOGIKREGGLIAVILVCLISDVFLPIAGTLGVLDLSNA 75  
 Db 3 TPKVAGIQQNAAFLVQGTRRYYVIVVALCQGANGALIAAGVGERAALTHAHPNTLAR 62

QY 76 WGGIAYIILWFAVMAAKUDATNKVEAPOII 93  
 Db 63 FGGAFLIGVALLAARN 80

RESULT 12  
 S57940 YggA protein homolog - Aeromonas hydrophila  
 C;Species: Aeromonas hydrophila  
 C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
 C;Accession: S57940  
 R;Swift, S.; Fish, L.; Williams, P.; Stewart, G.S.A.B.; Reference number: S57938  
 A;Accession: S57940  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-211 <SWI>

RESULT 13  
 B82318 Lyb/Ygaa family protein VCO481 (imported) - Vibrio cholerae (strain N16961 serogroup O)  
 C;Species: Vibrio cholerae  
 C;Accession: B82318  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Brinkac, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.; Nature 406, 477-483, 2000  
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A;Reference number: A02035; MUID:2040683; PMID:10952301  
 A;Accession: B82318  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-211 <HEI>  
 A;Cross-references: UNIPROT:Q9KUN4; UNIPARC:UPI0000C2C83; GB:AE004134; GB:AE003852; NTI  
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C;Genetics:  
 A;Gene: VCO481  
 A;Map position: I  
 C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)

Query Match 18.7%; Score 116; DB 2; Length 211;  
 Best Local Similarity 26.7%; Pred. No. 0.0003; Mismatches 60; Indels 4; Gaps 1; Matches 31; Conservative 21; Mismatches 60; Indels 4; Gaps 1;

QY 6 IFTGLLIGASILLISIGPQNVVVIKOGIKREGGLIAVILVCLISDVFLPIAGTLGVLDLSNA 65  
 Db 5 ILLQGFSGATWIPIGRNQAVYLNDQIKRHHLTATCGYLDMDITITLGIFGGGALIS 64

QY 66 AAPIVLDIMRGGIAYIILWFAVMAAKUDATNKVEAPOII 121  
 Db 65 QNTSLIGVTLAGILFLGGYGLSLRNL---KPPQSESTANPMAGRKAVIFG 116

RESULT 14  
 DB8016 hypothetical protein BH2932 [imported] - Bacillus halodurans (strain C-125)  
 C;Species: Bacillus halodurans  
 C;Accession: D84016  
 C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A;Reference number: A83650; MUID:20512582; PMID:11058132  
 A;Accession: D84016  
 A;Molecule type: DNA  
 A;Status: preliminary  
 A;Cross-references: UNIPROT:Q9K8S1; UNIPARC:UPI0000C4058; GB:AP001517; GB:BA000004; NII  
 C;Genetics:  
 A;Gene: BH2932  
 C;Superfamily: hypothetical protein b1798

Query Match 17.6%; Score 109; DB 2; Length 210;  
 Best Local Similarity 32.1%; Pred. No. 0.0015;

Matches 36; Conservative 19; Mismatches 45; Indels 12; Gaps 5;  
 QY 2 VIMEIFITGILGLGSLLSLSTGPQNYLVIKOGI--KREGHIAVIVLCLSDVFLIAGT- 57  
 C;Species: Caulobacter crescentus  
 C;Date: 20-apr-2001 #sequence\_revision 20-apr-2001 #text\_change 09-Jul-2004  
 C;Accession: E87522  
 R;Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kollar,  
 N.; J.; Brmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A;Title: Complete Genome Sequence of Caulobacter crescentus.  
 A;Reference number: A87249; MUID:21173698; PMID:11259647  
 A;Accession: E87522  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-210 <STO>  
 A;Cross-references: UNIPROT:Q9AC37; UNIPARC:UP100000C6EE9; GB:AE005673; NID:91342119; E  
 C;Genetic  
 A;Gene: CC0029  
 C;Superfamily: hypothetical protein b1798  

Query Match 17.3%; Score 107; DB 2; Length 210;  
 Best Local Similarity 26.5%; Pred. No. 0.0024;  
 Matches 30; Conservative 25; Mismatches 46; Indels 12; Gaps 3;  
 C;Conservative  
 QY 7 PINGLIGASLILSISIGPONVLVKOGI--KREGHIAVIVLCLSDVFLIAGTGVLL 63  
 Db 7 WIAFTLVLCLSMALITPGPNNMLVNSRISICQGRWAGIVSLLTGAFFVVILCA-ALGITAL 65  
 QY 64 SNAPIVUDIMRGGIAVLLWFAVMAAKDAMTKVEAQIIETEPTVPPDTP 116  
 Db 66 LMAPIAYDLRLRGAGALYLAWLAWQATRPGGASPFQVRLL-----PKDSP 110

Search completed: July 19, 2006, 00:31:14  
 Job time : 42 secs

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

Copyright (c) 1993 - 2006 Biocceleration Ltd.	Gencore version 5.1.9									
Om protein - protein search, using sw model										
Run on: July 19, 2006, 00:22:17 ; Search time 298 Seconds	(without alignments)									
Sequence: 1 MVVMBIFITGSLLGASLLS.....BETEPTVPPDTPLGVFGGGH 124	384.906 Million cell updates/sec									
Scoring table: BLOSUM62										
Searched: Gapext 10.0 , Gapext 0.5										
Total number of hits satisfying chosen parameters: 2849598										
Minimum DB seq length: 0										
Maximum DB seq length: 200000000										
Post-processing: Minimum Match 0%										
Maximum Match 100%										
Listing first 45 summaries										
Database : UniProt-7.2:*										
1: uniprot_sprot:*										
2: uniprot_trembl:*										
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
Result No. Score	Query Match	Length	DB ID	Description	RESULT	1	Q4H475 CORGL	PRELIMINARY	PRT;	121 AA.
1 607 97.9	121 2	Q4H475 CORGL	Q4H475 CORGL	Q4H475, corynebacter	ID	Q4H475_CORGL	Q4H475	AC	DT	30-AUG-2005, integrated into UniProtKB/T-EMBL.
2 571 92.1	1 LYSE CORGL	233 1	Q4H476 CORGL	Q4H476 corynebacter	DR	Q4H476_CORGL	Q4H476	AC	DT	07-FEB-2006, entry version 1.
3 571 92.1	2 LYSE CORGL	233 2	Q4H476 CORGL	Q4H476 corynebacter	DR	Q4H476_CORGL	Q4H476	AC	DT	Mutant Lysine exporter protein.
4 389.5 62.8	228 1 LYSE CORGL	228 1 LYSE CORGL	Q4H476 CORGL	Q4H476 corynebacter	DR	Q4H476_CORGL	Q4H476	AC	GN	Name=LysE24,
5 271 43.7	228 1 LYSE CORGL	228 1 LYSE CORGL	Q4H476 CORGL	Q4H476 corynebacter	DR	Q4H476_CORGL	Q4H476	AC	OS	Corynebacterium glutamicum (Brevibacterium flava)
6 214 34.5	1 ARGO_ECOL	211 1 ARGO_ECOL	Q2M9R9 ECOLI	Q2M9R9 escherichia	DR	Q2M9R9_ECOLI	Q2M9R9	AC	OC	Bacteria; Actinobacteridae; Actinomycetales;
7 214 34.5	211 2 ARGO_ECOL	Q2M9R9 ECOLI	Q2M9R9 escherichia	Q2M9R9 escherichia	DR	Q2M9R9_ECOLI	Q2M9R9	AC	OC	Corynebacterineae; Corynebacteriaceae; Corynebacterium;
8 213 34.4	211 2 Q2M9R9 ECOLI	Q2M9R9 ECOLI	Q2M9R9 escherichia	Q2M9R9 escherichia	DR	Q2M9R9_ECOLI	Q2M9R9	AC	OX	NCBI TaxID=1718;
9 210 33.9	211 1 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	RN	NUCLEOTIDE SEQUENCE.
10 212 33.9	211 1 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	RT	Strain=ATCC 13869;
11 210 33.9	211 1 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	RT	"Functional expression of mutant lysE gene for production of L-lysine in Methylphilus methylotrophus."
12 210 33.9	211 1 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	RT	RT
13 205 33.1	211 2 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	Submitted (JAN 2005) to the EMBL/GenBank/DBJ databases
14 204 32.9	211 1 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>
15 204 32.9	211 1 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	Distributed under the Creative Commons Attribution-NonDerivs license
16 204 32.9	211 1 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	DR
17 200 32.3	211 1 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	EMBL; AB199585; BAE07189_1; -; Genomic_DNA.
18 199.5 32.2	205 1 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	GO; GO:005293; F:lysine permease activity; IEA.
19 199.5 32.2	205 1 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	GO; GO:006865; F:amino acid transport; IEA.
20 198 31.9	205 1 ARGO_ECOL	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	DR
21 194 31.3	203 2 Q3YX09 SHISS	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	DR
22 193.5 31.2	202 2 Q3YX09 SHISS	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	DR
23 191.5 30.9	200 2 Q3YX09 SHISS	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	DR
24 189 30.5	200 2 Q3YX09 SHISS	Q3YX09 SHISS	Q3YX09 shiella so	Q3YX09 shiella so	DR	Q3YX09_SHISS	Q3YX09	AC	CC	DR
25 189 30.5	202 2 Q2K7B0_RHET	Q2K7B0_RHET	Q2K7B0 rhizobium e	Q2K7B0 rhizobium e	DR	Q2K7B0_RHET	Q2K7B0	AC	CC	DR
26 187.5 30.2	203 2 Q2K7B0_RHET	Q2K7B0_RHET	Q2K7B0 rhizobium e	Q2K7B0 rhizobium e	DR	Q2K7B0_RHET	Q2K7B0	AC	CC	DR
27 187 30.2	200 2 Q2P34_PSEU2	Q2P34_PSEU2	Q2P34 pseudomonas	Q2P34 pseudomonas	DR	Q2P34_PSEU2	Q2P34	AC	CC	DR
28 186 30.0	221 2 Q2P34_PSEU2	Q2P34_PSEU2	Q2P34 pseudomonas	Q2P34 pseudomonas	DR	Q2P34_PSEU2	Q2P34	AC	CC	DR
29 185 29.8	203 2 Q2P34_PSEU2	Q2P34_PSEU2	Q2P34 pseudomonas	Q2P34 pseudomonas	DR	Q2P34_PSEU2	Q2P34	AC	CC	DR
30 183 29.5	200 2 Q2P34_PSEU2	Q2P34_PSEU2	Q2P34 pseudomonas	Q2P34 pseudomonas	DR	Q2P34_PSEU2	Q2P34	AC	CC	DR
31 183 29.5	205 2 Q2E15_DESVD	Q2E15_DESVD	Q2E15 pseudomonas	Q2E15 pseudomonas	DR	Q2E15_DESVD	Q2E15	AC	CC	DR

RESULT 2

1 MEIFITGLLGLASLLSIGPQNLVKGKREGGLIAVLLVCLSDWFLIAGTGVDLL 63

1 MEIFITGLLGLASLLSIGPQNLVKGKREGGLIAVLLVCLSDWFLIAGTGVDLL 60

64 SNAPIVLDINRWGKJAYLWFAVMKAQDANTKVEAPQTEETEPTVPPDTPLGVFGGG 123

61 SNAPIVLDINRWGKJAYLWFAVMKAQDANTKVEAPQTEETEPTVPPDTPLGVFGGG 120

15-JUL-1998, integrated into UniProtKB/Swiss-Prot.

DT	14-AUG-2001	sequence version 2.
DT	07-MAR-2005	entry version 38.
DE	Lysine exporter protein.	
GN	Name=LySE; Order=locusNames=CgI1262, cgI1424;	
OS	Corynebacterium glutamicum (Brevibacterium flavum).	
OC	Bacteria; Actinobacteria; Actinomycetales;	
OC	Corynebacterineae; Corynebacteriaceae; Corynebacterium.	
OC	NCBI_TaxID=1718;	
RN		
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND FUNCTION.	
RC	STRAIN=RL127;	
RL		
RX	MEDLINE=97126810; PubMed=8917104; Vrijic M.M., Sahn H., Eggeling L.; "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ." Mol. Microbiol. 22:815-826(1996).	
RN		
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC	STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025; MEDLINE=2283012; PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8; [1]	
RN	"Complete genomic sequence of <i>Corynebacterium glutamicum</i> ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.	
RT	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC	STRAIN=ATCC 13869;	
RL		
RX	Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M., Egeling L., Gaigalat L., Goeckner A., Hartmann M., Ruthmacher K., Kraemer R., Linke B., McHardy A.C., Meyer P., Mockel B., Pfefferle W., Puhler A., Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegraebe I., Tauch A.; "The complete <i>Corynebacterium glutamicum</i> ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins." J. Biotechnol. 104:5-25(2003).	
RT	"The complete <i>Corynebacterium glutamicum</i> ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins." J. Biotechnol. 104:5-25(2003).	
CC	- - - - - FUNCTION: Involved in the efflux of excess of L-lysine. This is necessary to control the intracellular L-lysine level.	
CC	- - - - - SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass membrane protein.	
CC	- - - - - SIMILARITY: Belongs to the LySE/argO transporter (TC 2.A.75)	
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>	
CC	Distributed under the Creative Commons Attribution-NonDerivs License	
CC		
DR	EMBL: X96471; CA65324.2; -; Genomic DNA.	
DR	EMBL: BA00036; BAB98055.1; ALT INIT; Genomic_DNA.	
DR	EMBL: BX27151; CAP19651; -; Genomic_DNA.	
DR	GenomeReviews; BX927147_GR; cgI4242.	
DR	GenomeReviews; BA00056_GR; CgI11262.	
DR	InterPro; IPR04777; LySE exporter.	
DR	InterPro; IPR01123; LySE.	
DR	Pfam; PF01810; LySE; 1.	
DR	TIGRFAMS; TIGR00948; 2a75; 1.	
SQ	SEQUENCE: 233 AA; 25082 MN; F5FD9B1ACAD11D13 CRC64;	
Query Match	92.1%; Score 571; DB 2; Length 233; Best Local Similarity 100.0%; Pred. No. 3.2e-46; Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
FT	CHAIN 1; Complete proteome; Inner membrane; Membrane; Transporter; Lysine exporter protein.	
FT	/PRID=PRO_0000204157.	
FT	TRANSMEM 3 23 Potential.	
FT	TRANSMEM 35 55 Potential.	
FT	TRANSMEM 66 86 Potential.	
FT	TRANSMEM 144 164 Potential.	
FT	TRANSMEM 177 197 Potential.	
FT	TRANSMEM 213 233 Potential.	
SQ	SEQUENCE: 233 AA; 25082 MN; F5FD9B1ACAD11D13 CRC64;	
RESULT 4		
LYSE-COREF		
ID	LYSE-COREF	
AC	QBQCM4;	
DT	01-NOV-2002; integrated into UniProtKB/Swiss-Prot.	
DT	01-NOV-2002; sequence version 2.	
DT	07-MAR-2006; entry version 24.	
DE	Lysine exporter protein.	
GN	Name=LySE; Order=locusNames=CEI357;	
OS	Corynebacterium efficiens.	
OC	Bacteria; Actinobacteria; Actinomycetales;	
OC	Corynebacterineae; Corynebacteriaceae; Corynebacterium.	
OC	NCBI_TaxID=172794;	
RN		
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].	
RC	STRAIN=IS-3314 / AJ 12310 / DSM 44549 / JCM 11189;	
RA	Itaya H., Kimura E., Kawahara Y., Sugimoto S.;	
RT	"LySE, Lysine of <i>Corynebacterium</i> efficiens"; Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.	
RL		

RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RA STRAIN=YSG314 / AJ\_12310 / DSM 44549 / JCM 11189;  
 RT MEDLINE=22723752; PubMed=1284036; DOI=10.1101/gr.1285603;  
 RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,  
 RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,  
 RA Gojobori T.,  
 RT "Comparative complete genome sequence analysis of the amino acid  
 RT replacements responsible for the thermostability of Corynebacterium  
 RT efficient".  
 RL Genome Res. 13:1572-1579(2003).  
 CC -!- FUNCTION: Involved in the efflux of excess of L-lysine. This is  
 necessary to control the intracellular L-lysine level (By  
 similarity).  
 CC -!- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass  
 membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to the LysE/argo transporter (TC 2.A.75)  
 family.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
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 CC  
 DR EMBL: BA000313; BABB8827\_1; ALT-INIT; Genomic\_DNA.  
 DR EMBL: BA000315; BACB18167\_1; ALT-INIT; Genomic\_DNA.  
 DR GenomeReviews: BA000315; GR; CSE1357.  
 DR BiGGC; CEF196164; CSE1357-MONOMER; -.  
 DR InterPro; IPR001123; LysE.  
 DR Pfam; PF01810; LysE; 1.  
 KW Complete proteome; Membrane; Transmembrane; Transport;  
 FT CHAIN 1 228 Lysine exporter protein.  
 FT TRANSMEM 3 23 /FTID=PRO\_0000204156.  
 FT TRANSMEM 37 57 Potential.  
 FT TRANSMEM 66 86 Potential.  
 FT TRANSMEM 139 159 Potential.  
 FT TRANSMEM 172 192 Potential.  
 FT TRANSMEM 208 228 Potential.  
 FT TRANSMEM 228 AA; 24374 MW; 68FB379A8380EDA7 CRC64;  
 SQ SEQUENCE 62 8%; Score 389 5; DB 1; Length 228;  
 Best local similarity 65 8%; Pred. No. 6.8e-29;  
 Matches 79; Conservative 15; Mismatches 21; Indels 5; Gaps 2;  
 Qy 4 MEIFITGLLIGASLLSIGRQVNLVIKOGIKREGGLIAVLVCLISDVPIFLAGTLGVLL 63  
 Db 1 MEIFITGLLIGASLLSIGRQVNLVIKOGIKREGGLIAVLVCLISDVPIFLAGTLGVLL 60  
 Qy 64 SNAAPIVLUDMRWGGIAYLILWFAVMAKDAMTNKVEAPQIETEPTVPTVDPDPLGFGG 123  
 Db 61 SDTAPILIDPLIRWCGIAYLILWFAVMAKDAMTNKVEAPQIETEPTVPTVDPDPLGFGG 115  
 RESULT 5  
 LYSE\_CORDI  
 ID LYSE\_CORDI STANDARD: PRT; 228 AA.  
 AC 06NHP1;  
 DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-MAR-2006, entry version 10.  
 DE Lysine exporter protein.  
 GN Name=LysE; Order=eduNames=DIP1091;  
 OS Corynebacterium diphtheriae;  
 OC Bacteria; Actinobacteria; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 NCBI\_TaxID=1717;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Biotype gravis / NCTC 31329;  
 RX MEDLINE=2295543; PubMed=1602910; DOI=10.1093/nar/gkg874;  
 RA Cerdillo-Tarraga A.-M., Efstathiou A., Dover L.G., Holden M.T.G.,  
 RA Paillie M.J., Bentley S.D., Berra G.S., James K.D.,  
 RA De Zoya A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,  
 RA Hamlin N., Holroyd S., Jagger K., Moule S., Quail M.A.,  
 CC -!- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass  
 membrane protein (By similarity).  
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 CC  
 DR EMBL: BX48357; CABE9614\_1; -; Genomic\_DNA.  
 DR GenomeReviews: BX248353; GR; DIP1091.  
 DR BiGGC; CDIP177; DIP1091-MONOMER; -.  
 DR InterPro; IPR001123; LysE.  
 DR Pfam; PF01810; LysE; 1.  
 KW Complete proteome; Inner membrane; Membrane; Transmembrane; Transport;  
 FT CHAIN 1 228 Lysine exporter protein.  
 FT TRANSMEM 4 26 /FTID=PRO\_0000204155.  
 FT TRANSMEM 38 60 Potential.  
 FT TRANSMEM 65 87 Potential.  
 FT TRANSMEM 139 161 Potential.  
 FT TRANSMEM 171 193 Potential.  
 FT TRANSMEM 205 227 Potential.  
 SQ SEQUENCE 228 AA; 24662 MW; 6CS5ADD07CB3ADEF CRC64;  
 Qy 4 MEIFITGLLIGASLLSIGRQVNLVIKOGIKREGGLIAVLVCLISDVPIFLAGTLGVLL 63  
 Db 1 MSAITAGFLNGLISLIVGPNQNLITRQGKIKREGGLIPVILFGTAGVG 60  
 Qy 64 SNAAPIVLUDMRWGGIAYLILWFAVMAKDAMTNKVEAPQIETEPTVPTVDPDPLGFGG 119  
 Db 61 VDRAPIALVVLKMLGVAVLILFGTCFKAFAKFRHQQA LAVEOSEPVAYEPVADASSV 118  
 RESULT 6  
 ARGO\_ECOL6  
 ID ARGO\_ECOL6 STANDARD: PRT; 211 AA.  
 AC 08P55;  
 DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-MAR-2006, entry version 17.  
 DE Arginine exporter protein argo.  
 GN Name=argo; Order=eduNames=c301;  
 OS Escherichia coli 06.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 NCBI\_TaxID=217992;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=06\_H1 / CIPR073; ATCC 700928 / UPEC;  
 RX MEDLINE=2238824; PubMed=1471157; DOI=10.1073/pnas.252529799;  
 RA Welch R.A., Blunkett G. III, Redford P., Roesch P.,  
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
 RA Mayhew G.P., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.,  
 RT "Extensive mosaic structure revealed by the complete genome sequence  
 RT of uropathogenic Escherichia coli".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17720-17724(2002).  
 CC -!- FUNCTION: Involved in the export of arginine. Important to control  
 the intracellular level of arginine and the correct balance  
 between arginine and lysine (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass

CC membrane protein (By similarity).  
 CC -!- INDUCTION: Transcriptionally regulated by argP. Lysine has a  
 CC negative effect on the expression of argO (By similarity).  
 CC -!- SIMILARITY: Belongs to the *lysE/argO* transporter (TC 2.A.75).  
 CC family.

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 CC

CC EMBL: AE016766; AAN81494; GR; c3501.  
 CC GenoReviews; AE014075; GR; c3501.  
 CC BiOCYC; ECO119310; C301-MONOMER; -.

DR HAWAP; MP\_01901; -; 1.  
 DR InterPro; IPR04777; LysE exporter.  
 DR InterPro; IPR001123; LysE.  
 DR Pfam; PF01810; LysE; 1.  
 DR TIGRFAMS; TIGR0048; 2a75; 1.  
 DR Amino-acid transport; Complete proteome; Inner membrane; Membrane;  
 KW Transmembrane; Transport.  
 FT CHAIN 1 211 Arginine exporter Protein argO.  
 FT /FTid=PRO\_0000204160.  
 FT TRANSMEM 1 21 Potential.  
 FT TRANSMEM 22 36 Cytoplasmic (Potential).  
 FT TRANSMEM 37 57 Periplasmic (Potential).  
 FT TOPO\_DOM 58 67 Potential.  
 FT TRANSMEM 68 88 Cytoplasmic (Potential).  
 FT TRANSMEM 89 110 Potential.  
 FT TOPO\_DOM 111 131 Periplasmic (Potential).  
 FT TRANSMEM 132 145 Potential.  
 FT TOPO\_DOM 147 167 Cytoplasmic (Potential).  
 FT TRANSMEM 168 181 Periplasmic (Potential).  
 FT TRANSMEM 182 202 Potential.  
 FT TOPO\_DOM 203 211 AA; 23174 MW; 5F22D05A3A8FB0D73 CRC64; Sequence 211 AA; 23174 MW; 5F22D05A3A8FB0D73 CRC64;

Query Match 34.5%; Score 214; DB 1; Length 211;  
 Best Local Similarity 35.8%; Pred. No. 3.7e-12; Mismatches 41; Indels 18; Gaps 3;  
 Matches 48; Conservative 27; MisMatches 41; Indels 18; Gaps 3;

Qy 7 FITGGLLIGASLLSISGPOVNLVKGKIGRKGGLAVLVLCLISDVFLFIAQTGLGVDDLSNA 66  
 Db 5 YFOGLALGAMWLPQGPQAFVQNGIRQYHIMALLCAISDVFLVLCIGIFGGSALLMQ 64

Qy 67 APIVLDIMMRGGIAYLILWFAVMKAADKAMTKVE--APQIIE-----TEPT 110  
 Db 65 SPWLLALVTVGGVAFLLWYGGFAKFTAMSNIELASAEVLKQGRWKIATMLAVTLNPH 124

Qy 67 APIVLDIMMRGGIAYLILWFAVMKAADKAMTKVE--APQIIE-----TEPT 110  
 Db 111 VPDDT--PLGVFGG 122

Qy 65 SPWLLALVTVGGVAFLLWYGGFAKFTAMSNIELASAEVLKQGRWKIATMLAVTLNPH 124  
 Db 125 VVLLTFVVLGSLGG 138

RESULT 8  
 ARGO\_ECOLI STANDARD; PRT; 211 AA.  
 ID ARGO\_ECOLI STANDARD;  
 AC P11677;  
 DT 01-OCT-1999, integrated into UniProtKB/Swiss-Prot.  
 DT 01-OCT-1999, sequence version 2.  
 DT 07-MAR-2006, entry version 55.  
 DE Arginine exporter protein argO;  
 GN Name=argO; OrderedLocusNames=b2923;  
 OS Escherichia coli.  
 OC Bacterii; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OC NCBI\_TaxID=562;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=K12 / MG155;  
 RX MEDLINE-97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glaser J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davil N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474 (1997).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 15-211.  
 RC STRAIN=K12 / CS520;  
 RX MEDLINE-89313302; PubMed=2246007;  
 RA Alefournier P.R., Perham R.N.;  
 RT "Identification, molecular cloning and sequence analysis of a gene  
 RT cluster encoding the class II fructose 1,6-biphosphate aldolase, 3-  
 RT phosphoglycerate kinase and a putative second glyceraldehyde 3-  
 RT phosphate dehydrogenase of *Escherichia coli*.";  
 RL Mol. Microbiol. 37:723-732 (1999).  
 RN [3]  
 RP FUNCTION;  
 RC STRAIN=K12;  
 RX PubMed=15152422; DOI=10.1128/JB.186.11.3539-3546.2004;  
 RA Nandineni M.R., Gowri-Shankar J.;  
 RT "Evidence for an arginine exporter encoded by ygga (argO) that is  
 RT regulated by the lysR-type transcriptional regulator ArgP in  
 RT *Escherichia coli*.";  
 RL J. Bacteriol. 186:3539-3546 (2004).

RN [4]  
 RP TOPOLOGY.  
 RC STRAIN=K12 / MG1655;  
 RX PubMed=1591996; DOI=10.1126/science.1109730;  
 RA Daley D.O., Rapp M., Graneich E., Meien K., Drew D., von Heijne G.;  
 RT Bacterial topology analysis of the *Escherichia coli* inner membrane  
 proteome.";  
 RL *Science* 308:1321-1323(2005).  
 CC -!- FUNCTION: Involved in the export of arginine. Important to control  
 the intracellular level of arginine and the correct balance  
 between arginine and lysine. May also be involved in the export of  
 canavanine (a plant-derived antimetabolite).  
 CC -!- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass  
 membrane protein.  
 CC -!- INDUCTION: Transcriptionally regulated by argP in response to the  
 accumulation of intracellular arginine or canavanine. Lysine has a  
 negative effect on the expression of argo.  
 CC -!- SIMILARITY: Belongs to the LysEArgo transporter (TC 2.A.75)  
 CC family.  
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 DR EMBL: U00996; AAC75950.1; -; Genomic\_DNA.  
 DR EMBL: X1436; CR432607.1; -; Genomic\_DNA.  
 DR PIR: B65077; Q0C5A.  
 DR GenomeReviews: U0096\_GR; b2923.  
 DR EchoBASE; BBL148; -.  
 DR BioCyc; BioCyc:YGA-MONOMER; -.  
 DR LinkHub; P1167; -.  
 DR HAMAP; MF\_01901; -; 1.  
 DR InterPro; IPR00477; LysE.  
 DR InterPro; IPR00123; LysE.  
 DR PFam; PF0810; LysE; 1.  
 DR TIGRFAMS; TIGR00948; 2a75; 1.  
 DR Amino-acid transport; Complete proteome; Inner membrane; Membrane;  
 KW Transmembrane; Transport; Arginine exporter Protein argo.  
 FT CHAIN 1 211 /FTID=PRO\_0000204158.  
 FT TRANSMEM 1 211 /FTID=PRO\_0000204158.  
 FT TOPO\_DOM 22 36 Cytoplasmic (Potential).  
 FT TRANSMEM 37 57 Potential.  
 FT TOPO\_DOM 58 67 Periplasmic (Potential).  
 FT TRANSMEM 68 88 Potential.  
 FT TOPO\_DOM 89 110 Cyttoplasmic (Potential).  
 FT TRANSMEM 111 131 Potential.  
 FT TOPO\_DOM 132 146 Periplasmic (Potential).  
 FT TRANSMEM 147 167 Potential.  
 FT TOPO\_DOM 168 178 Cytoplasmic (Potential).  
 FT TRANSMEM 179 199 Potential.  
 FT TOPO\_DOM 200 211 Periplasmic (Potential).  
 SQ SEQUENCE 211 AA; 23176 MW; 2DATE27BAA9BEC22 CRC64;  
 Query Match 34.4%; Score 213; DB 1; Length 211;  
 Best Local Similarity 43.0%; Pred. No. 4.6e-12;  
 Matches 40; Conservative 21; Mismatches 32; Indels 0; Gaps 0;  
 Qy 7 PFTGILGASLLSISGPQNVVVIKQIKREGSIAVAVLVLCLSDVFIAGTLGVLDLNSA 66  
 Db 5 YFOGLGLGAAMILPQGPONAFTVNNQGIRQHIMALLCAISDVLICAGIFGGSALLMQ 64  
 Qy 67 APIVIDLIMRKIGAYILWFAVMAKADMTNIVK 99  
 Db 65 SPWILLALVYTGQAVLFLWIGGAKFTAMSSNIE 97  
 RESULT 9 Q2M9R9\_ECOLI PRELIMINARY; PRT; 211 AA.  
 ID Q2M9R9\_ECOLI  
 AC Q2M9R9  
 DT 21-FEB-2006, integrated into UniProtKB/TREMBL.  
 DT 21-FEB-2006, sequence version 1.  
 DT 07-MAR-2006, entry version 2.  
 DE Arginine transporter.  
 GN Name=argO;  
 OS *Escherichia coli* W3110.  
 OC *Bacteriia*; *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*;  
 OC *Enterobacteriaceae*; *Escherichia*.  
 RX OC  
 RA OX NCBI\_TaxID=316407;  
 RN RN  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RA RX  
 RA Smith D.R., Calvo J.M.;  
 RT "Nucleotide sequence of the *E. coli* gene coding for dihydrofolate  
 reductase.";  
 RT Nucleic Acids Res. 8:2255-2274(1980).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RA RA  
 RA Sekiguchi T., Ortega-Cesena J., Nosch Y., Ohashi S., Tauda K.,  
 RA Kanaya S.;  
 RT "DNA and amino-acid sequences of 3-isopropylmalate dehydrogenase of  
 Bacillus coagulans. Comparison with the enzymes of *Saccharomyces  
 cerevisiae* and *Thermus thermophilus*";  
 RT Biochim. Biophys. Acta 867:36-44(1986).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RA Chen R., Sun Y., Stark T., Beattie W., Moses R.E.;  
 RT "Nucleotide sequence and deletion analysis of the *polB* gene of  
*Escherichia coli*";  
 RT DNA Cell Biol. 9:613-635(1990).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RA Smallshaw J.E., Keill R.A.;  
 RT "Cloning, nucleotide sequence and expression of the *Escherichia coli*  
 K-12 *pyrH* gene encoding UMP kinase";  
 RT Genetics (Life Sci. Adv.) 11:59-65(1992).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RA Hayashi K., Morooka N., Yamamoto Y., Fujita K., Isono K., Choi S.,  
 RA Ohtsubo E., Baba T., Wanner B.L., Mori H., Horuchi T., Keseiler T.M., Kosuge T.,  
 RA Riley M., Abe T., Arnaud M.B., Barlyn M.K., Blattner F.R.,  
 RA Chaudhuri R.R., Glasner J.D., Horuchi T., Keseiler T.M.,  
 RA Mori H., Perna N.T., Plunkett G. III, Rudd K.E., Serres M.H.,  
 RA Thomas G.H., Thomson N.R., Wishart D., Wanner B. L.;  
 RA "Escherichia coli K-12: a cooperatively developed annotation snapshot-  
 2005";  
 RT Nucleic Acids Res. 34:1-9 (2006).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX RX  
 RX PubMed=15397293; DOI=10.1093/nar/gkj150;  
 RA Riley M., Abe T., Arnaud M.B., Barlyn M.K., Blattner F.R.,  
 RA Chaudhuri R.R., Glasner J.D., Horuchi T., Keseiler T.M.,  
 RA Mori H., Perna N.T., Plunkett G. III, Rudd K.E., Serres M.H.,  
 RA Thomas G.H., Thomson N.R., Wishart D., Wanner B. L.;  
 RA "Escherichia coli K-12: a cooperatively developed annotation snapshot-  
 2005";  
 RT Nucleic Acids Res. 34:1-9 (2006).  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX RX  
 RX MEDLINE=97349980; PubMed=9205837; DOI=10.1093/nar/gkj150;  
 RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,  
 RA Itoch T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsubashi N.,  
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,  
 RA Oshima T., Oshima S., Saito N., Sampei G., Saito Y., Sivasundaram S.,  
 RA Tazami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,  
 RA Yamagata S., Horiochi T.;  
 RT "Construction of a contiguous 874-kb sequence of the *Escherichia coli*  
 -K12 genome corresponding to 50.0-68.8 min on the linkage map and  
 analysis of its sequence features.";  
 RL DNA Res. 4:91-113(1997).  
 [8] Res. 4:91-113(1997).

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=97251358; PubMed=9097040; DOI=10.1093/dnareg/3.6.379;  
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
 RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,  
 RA Mizobuchi K., Mori T., Motomura K., Nakada S., Nakamura Y.,  
 RA Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,  
 RA Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,  
 RA Yamamoto Y., Horiochi T.;  
 RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome  
 corresponding to the 40.1-50.0 min region on the linkage map.;"  
 RL DNA Res. 3:379-392(1996).  
 RN [9]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=97251357; PubMed=9097039; DOI=10.1093/dnareg/3.6.363;  
 RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
 RA Kasai H., Kasimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
 RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,  
 RA Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,  
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiochi T.;  
 RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome  
 corresponding to the 28.0-40.1 min region on the linkage map.;"  
 RL DNA Res. 3:363-377(1996).  
 RN [10]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=97034878; PubMed=8940112; DOI=10.1074/jbc.271.49.31145;  
 RA Att E.A., Abelson J.N.;  
 RT "The 2'-5' RNA ligase of *Escherichia coli*. Purification, cloning, and  
 genomic disruption.";  
 RL J. Biol. Chem. 271:31145-31153(1996).  
 RN [11]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=97051202; PubMed=8905232; DOI=10.1093/dnareg/3.3.137;  
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto T., Inada T., Itoh T., Kajihara K., Kasai K., Kasimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,  
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiochi T.;  
 RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome  
 corresponding to the 12.7-28.0 min region on the linkage map.;"  
 RL DNA Res. 3:137-155(1996).  
 RN [12]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=94261430; PubMed=8202364;  
 RA Fujita N., Mori H., Yura T., Ishihama A.;  
 RT "Systematic sequencing of the *Escherichia coli* genome: analysis of the  
 2.4-4.1 min (110,917-193,643 bp) region.;"  
 RL Nucleic Acids Res. 22:1637-1639(1994).  
 RN [13]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=94240115; PubMed=8183897;  
 RA Janoi L., Shimizu T., Kaji A.;  
 RT "Ribosome recycling factor (ribosome releasing factor) is essential  
 for bacterial growth.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4249-4253(1994).  
 RN [14]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=94124004; PubMed=7904973; DOI=10.1016/0378-1119(93)90470-N;  
 RA Alilkann R., Gerard B.C., Court D., Dean M.C.;  
 RT "Cloning and organization of the *abc* and *mdl* genes of *Escherichia*  
 coli: relationship to eukaryotic multidrug resistance.";  
 RL Gene 136:231-236(1993).  
 RN [15]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=94018640; PubMed=8412634;  
 RA van Heeswijk W.C., Robbenberg M., Westerhoff H.V., Kahn D.D.;  
 RT "The genes of the glutamine synthetase adenylylation cascade are not  
 regulated by nitrogen in *Escherichia coli*.";  
 RL Mol. Microbiol. 9:443-458(1993).  
 RN [16]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=93259920; PubMed=8387990;  
 RA Zhao S., Sandt C.H., Feulner G., Vlazny D.A., Gray J.A., Hill C.W.;  
 RT "Rhs elements of *Escherichia coli* K-12: complex composites of shared  
 and unique components that have different evolutionary histories.;"  
 RL J. Bacteriol. 175:2759-2808(1993).  
 RN [17]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=93123180; PubMed=8419307;  
 RA Yamada M., Asaka S., Safer M.H. Jr., Yamada Y.;  
 RT "Characterization of the *gad* gene from *Escherichia coli* K-12 W3110 and  
 regulation of its expression.";  
 RL J. Bacteriol. 175:568-571(1993).  
 RN [18]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=93116053; PubMed=1474579;  
 RA Cormack R.S., Mackie G.A.;  
 RT "Structural requirements for the processing of *Escherichia coli* 5 S  
 ribosomal RNA by RNase E in vitro.";  
 RL J. Mol. Biol. 228:1078-1090(1992).  
 RN [19]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=9309412; PubMed=1459951;  
 RA Garvais F.G., Drapeau G.R.;  
 RT "Identification, cloning, and characterization of *rcsF*, a new  
 regulator gene for exopolysaccharide synthesis that suppresses the  
 RT division mutation *frsZ84* in *Escherichia coli* K-12.";  
 RL J. Bacteriol. 174:8016-8022(1992).  
 RN [20]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=93077430; PubMed=1447125;  
 RA Yamada K., Ogura T., Niki H., Hiraga S.;  
 RT "Identification and characterization of the *smbA* gene, a suppressor of  
 the *mukB* null mutant of *Escherichia coli*.";  
 RL J. Bacteriol. 174:7517-7526(1992).  
 RN [21]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=93011013; PubMed=1396599;  
 RA Condon C., Phillips J., Fu Z.Y., Squires C., Squires C.L.;  
 Query Match 34.4%; Score 213; DB 2; Length 211;  
 Best Local Similarity 43.0%; Pred. No. 4-6-12;  
 Matches 40; Conservative 21; Mismatches 32; Indels 0; Gaps 0;  
 Ov 7 FITGLLIGASHLISLGPQNVVVIKOGIKRGLIAVLLVCLISDVTFLIAGTLGVPLNSA 66  
 Db 5 YFOGLALGAAMILPLGQPNQAFVNMQGIRQHIMIALLCAISDLVILACIGFGSALLQ 64

Ov 67 APIVLDIMMRKGIGAYIILWPAWMAKADMTKVE 99  
 Db 65 SPWLLALVTWGGVAFLLWYFGFAFKTAMSSNIE 97

RESULT 10  
 ID Q3YX19 SH3SS PRELIMINARY; PRT; 211 AA.  
 AC Q3YX19\_SH3SS  
 DT 27-SEP-2005, integrated into UniProtKB/TREMBL.  
 DT 27-SEP-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 5.  
 DB Hypothetical protein YGGA.

GN Name=yggA; OrderedLocusName=SSO\_3075; ORFNames=SSO\_3075;  
 OS Shigellla sonnei (strain SSO46).  
 OC **Bacteriia**; **Proteobacteria**; **Gammaproteobacteria**; **Enterobacteriales**;  
 OC **Enterobacteriaceae**; **Shigella**.  
 RN NCBI\_TAXID=300269;  
 RN RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX PubMed=16235786; DOI=10.1093/nar/gk1954;  
 RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,  
 RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,  
 RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,  
 RA Qiang B., Hou Y., Yu J., Jin Q.;  
 RT "Genome dynamics and diversity of *Shigella* species, the etiologic  
 RT agents of bacillary dysentery.";  
 CC Nucleic Acids Res. 33:6443-6458 (2005).  
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 CC  
 CC EMBL; CP000038; AA289663.1; ; Genomic\_DNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005293; F:lysine permease activity; IEA.  
 DR GO; GO:006865; P:lysine acid transport; IEA.  
 DR InterPro; IPR003016; Lipoyl\_BS.  
 DR InterPro; IPR004777; Lys exporter.  
 DR Pfam; PF01810; LYSE\_1.  
 DR PROSITE; TIGR00948; 2a75; 1.  
 DR PROSITE; TIGR00948; 2a19; Lipoyl; UNKNOWN 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 211 AA; 23174 MW; DC946439D96EB920 CRC64;  
 Query Match 34.2%; Score 212; DB 2; Length 211;  
 Best Local Similarity 35.1%; Pred. No. 5.7e-12;  
 Matches 47; Conservative 28; Mismatches 18; Gaps 3;  
 Result 11  
 ARGO\_ECO57  
 ID ARGO\_ECO57 STANDARD; PRT; 211 AA.  
 AC Q8XJ0; Q7AYA8;  
 DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 07-MAR-2006, entry version 3.  
 DE Arginine exporter protein argo.  
 GN Name=argO; OrderedLocusNames=4260, ECs31794;  
 OS Escherichia coli O157:H7;  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=21074935; PubMed=11205551; DOI=10.1093/nar/gk1954;  
 RA Perma N.T., Plunkett G. III., Burland V., Mau B., Glazner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Grigor J., Kirkpatrick H.A.,  
 RA Postai G., Hackett J.J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grotbeck E.J., Davis N.W., Lin A., Dimlanta E.T., Potamoussis K.,  
 RA Apodaca J., Arantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RA Welch R.A., Blattner F.R.;  
 RN RP "Genome sequence of enterohaemorrhagic *Escherichia coli* 0157:H7.";  
 RN Nature 409:529-533 (2001).  
 RN [2]  
 RN RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX STRAIN=0157:H7 / Sakai / RIMD 050952 / EHEC;  
 RX MEDLINE=21156231; PubMed=11205551; DOI=10.1093/nar/gk1954;  
 RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*  
 RT 0157:H7 and genomic comparison with a laboratory strain K-12.";  
 RL DNA Res. 8:11-22 (2001).  
 CC -!- FUNCTION: Involved in the export of arginine. Important to control  
 CC the intracellular level of arginine and the correct balance  
 CC between arginine and lysine (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass  
 CC membrane protein (By similarity).  
 CC -!- INDUCTION: Transcriptionally regulated by argP. Lysine has a  
 CC negative effect on the expression of argO (By similarity).  
 CC -!- SIMILARITY: Belongs to the lysB/argO transporter (TC 2.A.75)  
 CC family.  
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 CC  
 DR EMBL; AB005174; AAGS8049\_1; ; Genomic\_DNA.  
 DR BioCyc; EC018334-1; ECS3794-MONOMER; -.  
 DR InterPro; IPR004777; Lys exporter.  
 DR PIR; B91103; B91103.  
 DR PIR; B85948; B85948.  
 DR GenomeReviews; BA000007\_GR; ECS3794.  
 DR GenomicReviews; AB005174\_GR; 24260.  
 DR HAMAP; MF\_01901; ; 1.  
 DR InterPro; IPR001123; LYSE.  
 DR Pfam; PF01810; LYSE\_1.  
 DR PROSITE; TIGR00948; 2a75; 1.  
 DR Amino-acid transport; Complete proteome; Inner membrane; Membrane;  
 KW Transmembrane; Transport.  
 FT CHAIN 1 211 Arginine exporter protein argO.  
 FT /PRD=PRO 000004159.  
 FT TRANSMEM 1 21 Arginine exporter protein argO.  
 FT TRANSMEM 22 36 Potential.  
 FT TRANSMEM 37 57 Cytoplasmic (Potential).  
 FT TOPO\_DOM 58 67 Potential.  
 FT TRANSMEM 68 88 Periplasmic (Potential).  
 FT TOPO\_DOM 89 110 Potential.  
 FT TRANSMEM 111 131 Cytoplasmic (Potential).  
 FT TOPO\_DOM 132 146 Periplasmic (Potential).  
 FT TRANSMEM 147 167 Potential.  
 FT TOPO\_DOM 168 181 Cytoplasmic (Potential).  
 FT TRANSMEM 182 202 Potential.  
 FT TOPO\_DOM 203 211 Periplasmic (Potential).  
 SQ SEQUENCE 211 AA; 23202 MW; 4422D078B182266C CRC64;  
 Query Match 33.9%; Score 210; DB 1; Length 211;  
 Best Local Similarity 35.1%; Pred. No. 8.8e-12;  
 Matches 47; Conservative 27; Mismatches 42; Indels 18; Gaps 3;  
 Result 11  
 ARGO\_ECO57  
 ID ARGO\_ECO57 STANDARD; PRT; 211 AA.  
 AC Q8XJ0; Q7AYA8;  
 DT 11-OCT-2004, sequence version 3.  
 DT 07-MAR-2006, entry version 20.  
 DE Arginine exporter protein argo.  
 GN Name=argO; OrderedLocusNames=4260, ECs31794;  
 OS Escherichia coli O157:H7;  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=21074935; PubMed=11205551; DOI=10.1093/nar/gk1954;  
 RA Perma N.T., Plunkett G. III., Burland V., Mau B., Glazner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Grigor J., Kirkpatrick H.A.,  
 RA Postai G., Hackett J.J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grotbeck E.J., Davis N.W., Lin A., Dimlanta E.T., Potamoussis K.,  
 RA Apodaca J., Arantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
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 RN [2]  
 RN RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX STRAIN=0157:H7 / Sakai / RIMD 050952 / EHEC;  
 RX MEDLINE=21156231; PubMed=11205551; DOI=10.1093/nar/gk1954;  
 RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,  
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 CC family.  
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 CC  
 DR EMBL; AB005174; AAGS8049\_1; ; Genomic\_DNA.  
 DR BioCyc; EC018334-1; ECS3794-MONOMER; -.  
 DR InterPro; IPR004777; Lys exporter.  
 DR PIR; B91103; B91103.  
 DR PIR; B85948; B85948.  
 DR GenomeReviews; BA000007\_GR; ECS3794.  
 DR GenomicReviews; AB005174\_GR; 24260.  
 DR HAMAP; MF\_01901; ; 1.  
 DR InterPro; IPR001123; LYSE.  
 DR Pfam; PF01810; LYSE\_1.  
 DR PROSITE; TIGR00948; 2a75; 1.  
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 KW Transmembrane; Transport.  
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 FT TOPO\_DOM 58 67 Periplasmic (Potential).  
 FT TRANSMEM 68 88 Potential.  
 FT TOPO\_DOM 89 110 Cytoplasmic (Potential).  
 FT TRANSMEM 111 131 Periplasmic (Potential).  
 FT TOPO\_DOM 132 146 Cytoplasmic (Potential).  
 FT TRANSMEM 147 167 Periplasmic (Potential).  
 FT TOPO\_DOM 168 181 Cytoplasmic (Potential).  
 FT TRANSMEM 182 202 Periplasmic (Potential).  
 FT TOPO\_DOM 203 211 Cytoplasmic (Potential).  
 SQ SEQUENCE 211 AA; 23202 MW; 4422D078B182266C CRC64;  
 Query Match 33.9%; Score 210; DB 1; Length 211;  
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 Matches 47; Conservative 27; Mismatches 42; Indels 18; Gaps 3;  
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 ID ARGO\_ECO57 STANDARD; PRT; 211 AA.  
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 DT 07-MAR-2006, entry version 20.  
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 RX MEDLINE=21074935; PubMed=11205551; DOI=10.1093/nar/gk1954;  
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 RA Rose D.J., Mayhew G.F., Evans P.S., Grigor J., Kirkpatrick H.A.,  
 RA Postai G., Hackett J.J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grotbeck E.J., Davis N.W., Lin A., Dimlanta E.T., Potamoussis K.,  
 RA Apodaca J., Arantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RA Welch R.A., Blattner F.R.;  
 RN RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX STRAIN=0157:H7 / Sakai / RIMD 050952 / EHEC;  
 RX MEDLINE=21156231; PubMed=11205551; DOI=10.1093/nar/gk1954;  
 RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*  
 RT 0157:H7 and genomic comparison with a laboratory strain K-12.";  
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 CC the intracellular level of arginine and the correct balance  
 CC between arginine and lysine (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass  
 CC membrane protein (By similarity).  
 CC -!- INDUCTION: Transcriptionally regulated by argP. Lysine has a  
 CC negative effect on the expression of argO (By similarity).  
 CC -!- SIMILARITY: Belongs to the lysB/argO transporter (TC 2.A.75)  
 CC family.

RESULT 12		SEQ	SEQUENCE	211 AA;	23202 MW;	4422D078B182266C CRC64;
ARGO_SHFL		Query	FTGLLIGASLLSISGPNVLYKQGKREGGLIAVLVCLISDVLFLACTLGVDLNSA	33.94%;	Score 210;	DB 1;
ID	Q7UBP8; Q83J77;	Match	YFQGUDIGAMILPLGPQNAFVFMNQGIRYHIMALLCRISDLVLLICAGIFGGSALMQ	35.14%;	Length 211;	
AC	STANDARD;	Best Local Similarity	64	Pred. No. 8	DB 1;	
DT	04-JAN-2005, integrated into UniProtKB/Swiss-Prot.	Matches	7	8e-12;	Length 211;	
DT	01-OCT-2003, sequence version 1.	47		27;	Matches 42;	
DT	07-MAR-2006, entry version 15.	Conservative		18;	Indels 18;	
DE	Arginine exporter Protein argo.	Mismatches		3;	Gaps 3;	
GN	Name=argO; Order=locusNames=SFF908; S3108;					
OS	Shigella flexneri.					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;					
OC	Enterobacteriaceae; Shigella.					
OX	NCBI_TaxID=623;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].					
RC	STRAIN=301 / Serotype 2a;					
RX	MEDLINE=22222406; PubMed=12384590; DOI=10.1093/nar/gkf566;					
RA	Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,					
RA	Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,					
RA	Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,					
RA	Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,					
RA	Yu J.;					
RT	"Genome sequence of <i>Shigella flexneri</i> 2a: insights into pathogenicity of <i>Escherichia coli</i> K12 and O157."					
RL	Nucleic Acids Res. 30:4432-4441 (2002).					
RN	[12]					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].					
RC	STRAIN=2457T / ATCC 700930 / Serotype 2a;					
RX	MEDLINE=22290274; PubMed=12704152;					
RA	DOI=10.1128/IAI.71.5.2785-2786.2003;					
RA	Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,					
RA	Fournier G., Mayhew G.F., Plunnett G. III, Rose D.J., Darling A.,					
RA	Mau B., Peng N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,					
RA	Schwartz D.C., Blattner F.R.;					
RT	"Complete genome sequence and comparative genomics of <i>Shigella flexneri</i> serotype 2a strain 2457T."					
RL	Infect. Immun. 71:2775-2786 (2003).					
CC	-!- FUNCTION: Involved in the export of arginine. Important to control the intracellular level of arginine and the correct balance between arginine and lysine (By similarity).					
CC	-!- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass membrane Protein (By similarity).					
CC	-!- SIMILARITY: Belongs to the <i>lysE</i> /argo transporter (TC 2.A.75) family.					
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>					
CC	Distributed under the Creative Commons Attribution-NonDerivs License					
CC						
DR	EMBL: AE005674; AACN4390.1; ALT INIT; Genomic_DNA.	Query	FTGLLIGASLLSISGPNVLYKQGKREGGLIAVLVCLISDVLFLACTLGVDLNSA	33.48%;	Score 207;	DB 2;
DR	EMBL: AE016988; AABP7561.1; -; Genomic_DNA.	Match	YFQGUDIGAMILPLGPQNAFVFMNQGIRYHIMALLCRISDLVLLICAGIFGGSALMQ	35.14%;	Length 211;	
DR	GenomeReviews; AE005747_GR; S3108.	Best Local Similarity	64	Pred. No. 1.7e-11;	DB 2;	
DR	HAMAP: MF_01901; -; 1.	Matches	7	TEPT 110	Length 211;	
DR	InterPro; IPR001777; Lys exporter.	Conservative				
DR	InterPro; IPR001123; LysE.	Mismatches	27;			
DR	PFam; PF01810; LysE; 1.	Indels	42;			
DR	TIGRFAMs; TIGR00948; 2a75; 1.	Gaps	18;			
KW	Amino-acid transport; Complete proteome; Inner membrane; Membrane; Transmembrane; Transport.	Score	207;			
FT	CHAIN 1 211	DB	5			
FT	Arginine exporter protein argo.	Qy	YFQGUDIGAMILPLGPQNAFVFMNQGIRYHIMALLCRISDLVLLICAGIFGGSALMQ	64		
FT	/FTID=PRO_000204167.	Db				
FT	Transmem	Qy	FTGLLIGASLLSISGPNVLYKQGKREGGLIAVLVCLISDVLFLACTLGVDLNSA	66		
FT	1 21	Db	7 APIVIDMRNGIAYILWFAAMDAKMTNKE--APOIIEE-----TEPT	67		
FT	Potential.	Qy	SPWLLALVTVGGVFLWLGFGFAKFTAMSSNIELASAEVLUKGWRKIIATMLAVTLNPH	65		
FT	Cyttoplasmic (Potential).	Db	111 VPDPT--PLGVFGG 122	125		
FT	22 36	Qy	132 VYLDIFVWLGSLGG 138	125		
FT	37 57	Db				
FT	Potential.					
FT	67 67					
FT	Periplasmic (Potential).					
FT	68 88					
FT	Potential.					
FT	89 110					
FT	Cyttoplasmic (Potential).					
FT	111 131					
FT	Potential.					
FT	132 146					
FT	Periplasmic (Potential).					
FT	147 167					
FT	Potential.					
FT	181 202					
FT	Cyttoplasmic (Potential).					
FT	202 211					
FT	Potential.					
FT	203 211					
FT	Periplasmic (Potential).					
PT	TRANSMEM	RESULT 14				
PT		ARGO_SALT1				

ID	ARGO_SAL1	STANDARD;	PRT;	211 AA.
AC	Q023W2; Q7C7C3;			
DT	11-OCT-2004, integrated into UniProtKB/Swiss-Prot.			
DT	01-MAR-2002, sequence version 1.			
DT	07-MAR-2006, entry version 18.			
DE	Arginine exporter protein argo.			
GN	Name=argO; OrderedLocusNames=STY3222, t2984;			
OS	Salmonella typhi.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Salmonella.			
OX	NCBI_TAXID=601;			
RN				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=TY2 / ATCC 700931;			
RX	Medline=22531367; PubMed=12644504;			
RA	DODI=10-1128/JB-185-7; 2330-2337; 2003;			
RA	Deng W., Liou S.-R., Blunkett G. III, Mayhew G. F., Rose D. J.,			
RA	Burland V., Kodoyanli V., Schwartz D.C., Blattner F.R.;			
RT	"Comparative genomics of <i>Salmonella enterica</i> serovar Typhi strains Ty2 and CT18."; J. Bacteriol. 185:2330-2337(2003).			
RL	--			
CC	-- FUNCTION: Involved in the export of arginine. Important to control the intracellular level of arginine and the correct balance between arginine and lysine (By similarity).			
CC	-- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass membrane protein (By similarity).			
CC	-- SIMILARITY: Belongs to the LysEArgo transporter (TC 2.A.75) family.			
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
DR	EMBL: AE014613; AA050536; 1; -; Genomic_DNA.			
DR	GenomeReviews; AL51338_GR; SC322.			
DR	GenomeReviews; AE014613_GR; t2984.			
DR	Biocyc; SENT020570; t2984-MONOMER; -.			
DR	HAMAP; MF_01901; -; 1.			
DR	InterPro; IPR004777; Lys exporter.			
DR	InterPro; IPR001123; LysE.			
DR	Pfam; PF01810; LysE; 1.			
DR	TIGR48; TIGR0948; 2a75; 1.			
KW	Amino-acid transport; Complete proteome; Inner membrane; Membrane; Transmembrane; Transport.			
FT	CHAIN 1 211			
FT	Arginine exporter protein argo.			
FT	/FTid=PRO_000204165;			
FT	Potential.			
FT	Cyttoplasmic (Potential).			
FT	Potential.			
FT	Periplasmic (Potential).			
FT	Potential.			
FT	Cyttoplasmic (Potential).			
FT	Potential.			
FT	Periplasmic (Potential).			
FT	Transmembrane.			
FT	TORO_DOM 89 110			
FT	Cyttoplasmic (Potential).			
FT	Potential.			
FT	Beriplasmic (Potential).			
FT	Potential.			
FT	Cyttoplasmic (Potential).			
FT	Potential.			
FT	Transmembrane.			
FT	TRANSMEM 1 21			
FT	Arginine exporter protein argo.			
FT	/FTid=PRO_000204163;			
FT	Transmembrane.			
FT	37 57			
FT	Potential.			
FT	Transmembrane.			
FT	111 131			
FT	Potential.			
FT	Transmembrane.			
FT	147 167			
FT	Potential.			
FT	Transmembrane.			
FT	179 199			
FT	Potential.			
FT	SEQUENCE 211 AA; 23339 MW; 64D6E6F0B3F1D0F CRC64;			
FT	Query Match Best Local Similarity 32.9%; Score 204; DB 1; Length 211; Matches 37; Conservative 25; Mismatches 35; Indels 0; Gaps 0;			
FT	1 MISYVFQEVAGAMLPIPLGPONAFVNMQGIRQHMLCALSDVLVLSAGIFGCSA 60			
FT	61 LIMQSPWLLALVYWGGAFLWVGFGLKTAMSSNL 97			
FT	63 LSNRAPPVLDIMWGGAYLFLRFAVMKADAMKNS 99			
FT	RESULTS 15			
FT	ID ARGO_SAL1			
FT	STANDARD;			
FT	PRT; 211 AA.			
FT	Query Match Best Local Similarity 33.1%; Score 205; DB 1; Length 211; Matches 37; Conservative 26; Mismatches 34; Indels 0; Gaps 0;			
FT	3 IMBIFRFLGSLSLUSIGRQVLYKQGIRKREGIAYLVCLISVFLPIAGTGLYD 62			
FT	1 MISYVFQEVAGAMLPIPLGPONAFVNMQGIRQHMLCALSDVLVLSAGIFGCSA 60			
FT	QY 63 LSNRAPPVLDIMWGGAYLFLRFAVMKADAMKNS 99			
FT	DB 61 LIMQSPWLLALVYWGGAFLWVGFGLKTAMSSNL 97			

Db	1 MISYYFGQFALGAAMLLPLGQNAFVNQGIRROQYHUMIAALCALSDLVJISAGF <small>GG</small> 60
QY	63 LSNAAPTVLDIINRGGTAYLILWFAVMKAQDAMNTKTE 99
Db	61 LLMQSPNLLALTVWGSGVAFLLWNYGFRALKTAMSNIE 97

Search completed: July 19, 2006, 00:30:30  
Job time : 302 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.9				
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Perfect score:	620				
Sequence:	1 MVIMEIFITGLLIGASLLS.....EEETEPTVPPDDTPLGVFGGHH 124				
Scoring table:	BLOSUM62				
Gapop 10.0 , Gapext 0.5					
Searched:	650591 seqs, 8753028 residues				
Total number of hits satisfying chosen parameters:	650591				
Minimum DB seq length: 0					
Maximum DB seq length: 2000000000					
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
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3:	/EMC_Celerra_SDSD3/ptodata/2/1aa/7_COMB pep:*				
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	584	94.2	236	2	US-09-105-117K-2
2	215	34.7	211	2	US-09-459-573-16
3	33.1	213	2	US-09-489-11845	
4	185	29.8	214	2	US-09-543-681A-4972
5	172.5	27.8	232	2	US-09-252-991A-4479
6	158	25.5	211	2	US-09-328-352-5737
7	112	18.1	211	2	US-09-902-50-9913
8	109	17.6	219	2	US-09-489-039A-7731
9	99.5	212	2	US-09-543-681A-4767	
10	93.5	15.1	235	2	US-09-328-352-8249
11	90.5	14.6	208	2	US-09-328-352-5111
12	88.5	14.3	212	2	US-09-459-573-12
13	88	14.2	211	2	US-09-489-039A-9608
14	86.5	14.0	205	2	US-09-489-039A-12661
15	86	13.9	206	2	US-09-252-991A-18746
16	86	13.9	260	2	US-09-252-991A-25992
17	83.5	13.5	210	2	US-09-328-352-4775
18	83	13.5	222	2	US-09-252-991A-26644
19	83	13.4	552	2	US-09-489-039A-7419
20	80.5	13.0	228	2	US-09-543-681A-6854
21	79.5	12.8	205	2	US-09-396-357-2
22	79.5	12.8	205	2	US-09-847-392-2
23	79.5	12.8	221	2	US-09-328-352-6659
24	79	12.7	250	2	US-09-543-881A-487
25	79	12.7	212	2	US-09-248-796A-20354
26	77.5	12.5	205	2	US-09-459-573-14
27	77.5	12.5	249	2	US-09-252-991A-25717
28	76.5	12.3	217	2	US-09-489-039A-8076
29	75	12.1	316	2	US-09-328-352-6071
30	74.5	12.0	1172	2	US-09-252-991A-16947
31	74	11.9	213	2	US-09-252-991A-22091
32	73	11.9	302	2	US-09-252-991A-22091
33	73.5	11.9	214	2	US-09-489-039A-9793
34	73.5	11.9	238	2	US-09-328-352-7122
35	73.5	11.9	464	2	US-09-489-039A-9621
36	73	11.8	222	2	US-09-328-352-6471
37	73	11.8	237	2	US-09-252-991A-21775
38	72.5	11.7	256	2	US-09-270-767-47525
39	72	11.6	211	2	US-09-252-991A-20747
40	72	11.6	427	2	US-09-721-870-115
41	72	11.6	434	2	US-09-721-870-117
42	72	11.6	446	2	US-09-602-787A-426
43	71.5	11.5	223	2	US-09-459-573-10
44	71.5	11.5	461	2	US-09-248-796A-23597
45	70.5	11.4	257	2	US-09-560-761B-12
ALIGNMENTS					
RESULT 1	US-09-105-117K-2				
;	Sequence 2, Application US/09105117K				
;	Patent No. 685805				
;	GENERAL INFORMATION:				
;	APPLICANT: Forschungszentrum Juelich GmbH; Marina Vrliic et al.				
;	TITLE OF INVENTION: Process for the microbial production of amino acids by boosted activity of export carriers				
;	FILE REFERENCE: 1				
;	CURRENT APPLICATION NUMBER: US/09/105,117K				
;	CURRENT FILING DATE: 1996-06-17				
;	PRIOR APPLICATION NUMBER: PCT/DE96/02485				
;	PRIOR FILING DATE: 1996-12-18				
;	NUMBER OF SEQ ID NOS: 5				
;	SOFTWARE: PatentIn Ver. 2.0				
;	SEQ ID NO: 2				
;	LENGTH: 236				
;	TYPE: PRT				
;	ORGANISM: Corynebacterium glutamicum				
;	FEATURE: (LySE)				
;	OTHER INFORMATION: (LySE)				
;	US-09-105-117K-2				
;	Query Match				
;	Best Local Similarity				
;	94.2%; Score 584; DB 2; length 236;				
;	Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
;	Sequence 16, Appli				
;	Sequence 1845, A				
;	Sequence 4972, AP				
;	Sequence 4972, AP				
;	Sequence 24479, A				
;	Sequence 5737, AP				
;	Sequence 9913, AP				
;	Db				
;	1 MVIMEIFITGLLIGASLLS.....EEETEPTVPPDDTPLGVFGGHH 118				
;	Qy				
;	61 DLSNAAPIVDIMRWGIGAYLWPAWAKDAMTKNVEAPQIETEPTVPPDDTPLGV 118				
;	Dy				
;	61 DLSNAAPIVDIMRWGIGAYLWPAWAKDAMTKNVEAPQIETEPTVPPDDTPLGV 118				
;	Db				
;	61 DLSNAAPIVDIMRWGIGAYLWPAWAKDAMTKNVEAPQIETEPTVPPDDTPLGV 118				
;	RESULT 2				
;	US-09-459-573-16				
;	Sequence 16, Application US/09459573				
;	Patent No. 697950				
;	GENERAL INFORMATION:				
;	APPLICANT: LIVSHITS, VITALY				
;	APPLICANT: ZAKATEVA, NATALIA				
;	APPLICANT: NAKANISHI, KAZUO				
;	APPLICANT: VENIAMINOVICH, VLADIMIR				
;	APPLICANT: TROSHIN, PETR				
;	APPLICANT: TOKHNOVA, IRINA				
;	TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACIDS				
;	FILE REFERENCE: 0010-1066-0				

CURRENT APPLICATION NUMBER: US/09/159,573  
 CURRENT FILING DATE: 1998-12-13  
 PRIOR APPLICATION NUMBER: RU981224016  
 PRIOR FILING DATE: 1998-12-30  
 PRIOR APPLICATION NUMBER: RU99104431  
 PRIOR FILING DATE: 1999-03-09  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 16  
 LENGTH: 211  
 TYPE: PRT  
 ORGANISM: Escherichia coli  
 US-09-459-573-16

Query Match 34.7%; Score 215; DB 2; Length 211;  
 Best Local Similarity 41.2%; Pred. No. 1.3e-19;  
 Matches 40; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

Qy 3 IMELFIFTGLLGLASLLSIGPQNLVVIKOGIKREGGLIAVLVCLISDVLFPIAGTLGLDL 62  
 Db 1 VFSVYFPQGLALGAMILPLGPQNAFVMMGIRRHIMTALLCAISDLVLCAGIFGGSA 60

Qy 63 LSNAPAPIVLDIMRWGGIAYILWFAVMAAKDAMTNKE 99  
 Db 61 LMQOSPWLALVWGGVAFLLWFGAFTKTMSSNIE 97

RESULT 3  
 US-09-489-039A-11845  
 Patent No. 6610836  
 Sequence 11845, Application US/09489039A

GENERAL INFORMATION:  
 APPLICANT: Gary Breton et. al  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 TITLE OF INVENTION: PNEUMONIA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 2/09 200401  
 CURRENT APPLICATION NUMBER: US/09/489, 039A  
 CURRENT FILING DATE: 2000-01-27  
 PRIOR APPLICATION NUMBER: US 60/117,747  
 PRIOR FILING DATE: 1999-01-29  
 NUMBER OF SEQ ID NOS: 14342  
 SEQ ID NO 11845  
 LENGTH: 213  
 TYPE: PRT  
 ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-11845

Query Match 33.1%; Score 205; DB 2; Length 213;  
 Best Local Similarity 37.4%; Pred. No. 2.7e-18;  
 Matches 37; Conservative 25; Mismatches 37; Indels 0; Gaps 0;

Qy 1 MVTMEBIFTGLLGLASLLSIGPQNLVVIKOGIKREGGLIAVLVCLISDVLFPIAGTLGLV 60  
 Db 1 IMFTTYFQGLALGAMILPLGPQNAFVMMGIRRHIMTALLCAISDLVLCAGIFGG 60

Qy 61 DILSNAAPIVLDIMRWGGIAYILWFAVMAAKDAMTNKE 99  
 Db 61 SALMQOSPWLALVWGGVAFLLWFGAFTKTMSSNIE 99

RESULT 4  
 US-09-543-681A-1972  
 Sequence 4972, Application US/09543681A  
 Patent No. 6655709  
 GENERAL INFORMATION:  
 APPLICANT: GARY BRETON  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 2/09 1.002-001  
 CURRENT APPLICATION NUMBER: US/09/543, 681A  
 CURRENT FILING DATE: 2000-04-05  
 PRIOR APPLICATION NUMBER: US 60/128,706  
 PRIOR FILING DATE: 1999-04-09

Query Match 29.8%; Score 185; DB 2; Length 214;  
 Best Local Similarity 36.0%; Pred. No. 1.1e-15;  
 Matches 36; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

Qy 3 IMELFIFTGLLGLASLLSIGPQNLVVIKOGIKREGGLIAVLVCLISDVLFPIAGTLGLDL 62  
 Db 8 MLTTFFQQCPFLSAMILPITAQNAFVQLOQSKKQYHMSAFLCALSDVILISGGVFGGSA 67

Qy 63 LSNAPAPIVLDIMRWGGIAYILWFAVMAAKDAMTNKE 99  
 Db 68 LUSQSEXYEMLLILWGGVAFLLWFGAFTKTMSSNIE 107

RESULT 5  
 US-09-252-991A-24479  
 Sequence 24479, Application US/09252991A  
 GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenstein et. al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSUEDOMONAS  
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 1/09 196-136  
 CURRENT APPLICATION NUMBER: US/09/252, 991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074, 788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094, 190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 24479  
 LENGTH: 232  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-24479

Query Match 27.8%; Score 172.5; DB 2; Length 232;  
 Best Local Similarity 35.7%; Pred. No. 5e-14;  
 Matches 35; Conservative 20; Mismatches 38; Indels 5; Gaps 1;

Qy 7 FITGLLGLASLLSIGPQNLVVIKOGIKREGGLIAVLVCLISDVLFPIAGTLGLDLNA 66  
 Db 37 YINGLILVAGLITATGQAQNVALQASLRLREHLSVALCFCDAVLVLSVFGGLAKLIL 96

Qy 67 APIVLDIMRWGGIAYILWFAVMAAKDAMTNKE 99  
 Db 97 NPTLIAIARWGGIAYILWFGKALLRARPDAIGNAE 134

RESULT 6  
 US-09-328-352-5737  
 Sequence 5737, Application US/09328352  
 Patent No. 6562958  
 GENERAL INFORMATION:  
 APPLICANT: Gary L. Breton et. al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: GTCC9-03PA  
 CURRENT APPLICATION NUMBER: US/09/328, 352  
 CURRENT FILING DATE: 1999-06-04  
 NUMBER OF SEQ ID NOS: 8252  
 SEQ ID NO 5737  
 LENGTH: 211  
 TYPE: PRT  
 ORGANISM: Acinetobacter baumannii  
 US-09-328-352-5737

Query Match 25.5%; Score 158; DB 2; Length 211;  
 Best Local Similarity 32.6%; Pred. No. 3.3e-12; Matches 29; Conservative 25; Mismatches 35; Indels 0; Gaps 0;

Qy 1 MVVMEIFITGULLGASLLSISGPOVNLVVIKQIKREGLAVLVLCLSDVFLFLAGTGV 60  
 Db 12 DLISNAPIVLDIMRMGGIAYLNAQAFVLUKQGLQQVFWCLTCAALSDSILACGVLG 71  
 Qy 61 DLISNAPIVLDIMRMGGIAYLNAQAFVLUKQGLQQVFWCLTCAALSDSILACGVLG 60  
 Db 72 AEINTASPLILITVAKILGATFLFVYGAKA 100

RESULT 7 US-09-902-540-9913  
 Sequence 9913, Application US/09902540  
 Patent No. 633447  
 GENERAL INFORMATION:  
 APPLICANT: Goldman, Barry S.  
 APPLICANT: Hinkle, Gregory J.  
 APPLICANT: Slater, Steven C.  
 APPLICANT: Wiegand, Roger C.  
 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
 FILE REFERENCE: 38-10(15849)B  
 CURRENT APPLICATION NUMBER: US/09/902, 540  
 CURRENT FILING DATE: 2001-07-10  
 PRIOR APPLICATION NUMBER: 60/217, 883  
 PRIOR FILING DATE: 2000-07-10  
 NUMBER OF SEQ ID NOS: 16825  
 SEQ ID NO 9913  
 LENGTH: 211  
 TYPE: PRT  
 ORGANISM: Myxococcus xanthus  
 US-09-902-540-9913

Query Match Best Local Similarity 25.6%; Score 112; DB 2; Length 211;  
 Matches 23; Conservative 26; Mismatches 35; Indels 6; Gaps 3;

Qy 16 SILLISIGPQNVLVIKQGK--KREGLAVLVLCLSDVFLFLAGTGVLDLISNAPIVLD 72  
 Db 17 ALILTPGPDTMFLVLRSLNSQGRKAGISALGLI-FVGCFPHIAAAFGSILATSAIAFS 75

RESULT 8 US-09-489-039A-7731  
 Sequence 7731, Application US/09489039A  
 Patent No. 6010836  
 GENERAL INFORMATION:  
 APPLICANT: Gary Breton et. al  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 FILE REFERENCE: 2709-200401  
 CURRENT APPLICATION NUMBER: US/09/489, 039A  
 CURRENT FILING DATE: 2000-01-27  
 PRIOR APPLICATION NUMBER: US 60/117, 747  
 PRIOR FILING DATE: 1999-01-29  
 NUMBER OF SEQ ID NOS: 14342  
 SEQ ID NO 7731  
 LENGTH: 219  
 TYPE: PRT  
 ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-7731

Query Match Best Local Similarity 27.5%; Score 109; DB 2; Length 219;  
 Matches 29; Conservative 20; Mismatches 45; Indels 10; Gaps 3;

Qy 17 VLTLYVAGVFLIVPGPNPFPFLVKTGAHGKVKGKYLAAVG-FIGDAVIMFLAFAGVATL 75  
 Db 64 SNAAPIVLDIMRMGGIAYLW---FAMAAKDAATMVKVEAP 101  
 Qy 76 IKTPVFLWVVRFLGATLWLGKMLYAVITORDGSDASAP 119

RESULT 9 US-09-543-681A-4767  
 Sequence 4767, Application US/09543681A  
 Patent No. 6605709  
 GENERAL INFORMATION:  
 APPLICANT: GARY BRETON  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 2709.1002-001  
 CURRENT APPLICATION NUMBER: US/09/543 681A  
 CURRENT FILING DATE: 2000-04-05  
 PRIOR APPLICATION NUMBER: US 60/128, 706  
 PRIOR FILING DATE: 1999-04-09  
 NUMBER OF SEQ ID NOS: 8344  
 SEQ ID NO 4767  
 LENGTH: 212  
 TYPE: PRT  
 ORGANISM: Proteus mirabilis  
 US-09-543-681A-4767

Query Match Best Local Similarity 27.6%; Score 99.5; DB 2; Length 212;  
 Matches 27; Conservative 26; Mismatches 38; Indels 7; Gaps 3;

Qy 5 EIFTGSLILGASLLSISGPOVNLVVIKQGK--REGLAVLVLCLSDVFLFLAGTGVGD 61  
 Db 17 DIFLSLAIIFSFVTSITFGPNMNLASSGNGFLKRTMPHAIGVSLGFVFLMLAVG-1GIG 75

RESULT 10 US-09-328-352-0249  
 Sequence 8249, Application US/09328352  
 Patent No. 6362958  
 GENERAL INFORMATION:  
 APPLICANT: Gary L. Breton et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 FILE REFERENCE: GTC99-03PA  
 CURRENT APPLICATION NUMBER: US/09/328, 352  
 CURRENT FILING DATE: 1999-06-04  
 NUMBER OF SEQ ID NOS: 8252  
 SEQ ID NO 8249  
 LENGTH: 235  
 TYPE: PRT  
 ORGANISM: Acinetobacter baumannii  
 US-09-328-352-0249

Query Match Best Local Similarity 27.3%; Score 93.5; DB 2; Length 235;  
 Matches 33; Conservative 21; Mismatches 54; Indels 13; Gaps 5;

Qy 3 IMEIITGULLGASLLSISGPOVNLVVIKQIKREGLAVLVLCLSDVFLFLAGTGV 59  
 Db 29 LSQIAFLGLIC-LANVLTDPNMYLISISS-OKKIAPISLGGVAVGVPYMLCASPG 86

Qy 60 VDLISNAPIVLDIMRMGGIAYLNAQAFVLUKQGLQQVFWCLTCAALSDSILACGVLG 119  
 Db 87 ITALVVAVPAVYAYDTIRIAGAMYLLWAKIRP---NAAPIFNVKDLAV-DSPLKL 138

Qy 120 F 120

Db 139 F 139

RESULT 11

US-09-328-352-511

; Sequence 5111; Application US/09328352

; Patent No. 6562358

; GENERAL INFORMATION:

; APPLICANT: Gary L. Bretton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; TITLE OF INVENTION: BRAMANNI FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC09-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 5111

; LENGTH: 208

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

; US-09-328-352-511

; Query Match 14.6%; Score 90.5; DB 2; Length 208;

; Best Local Similarity 24.3%; Pred. No. 0.0019; Matches 27; Conservatve 21; Mismatches 54; Indels 9; Gaps 3;

; APPLICANT: LIVSHITS, VITALY

; APPLICANT: ZAKATEVA, NATALIA

; APPLICANT: NAKANISHI, KAZUO

; APPLICANT: VENTIMINOVICH, VLADIMIR

; APPLICANT: TROSHIN, PETR

; APPLICANT: TOKHMAKOVA, IRINA

; TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACIDS

; FILE REFERENCE: 0010-1066-0

; CURRENT APPLICATION NUMBER: US/09/459,573

; CURRENT FILING DATE: 1999-12-13

; PRIOR APPLICATION NUMBER: RU98124016

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: RU99104431

; PRIOR FILING DATE: 1999-03-09

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12

; LENGTH: 212

; TYPE: PRT

; ORGANISM: Escherichia coli

; US-09-459-513-12

; Query Match 14.3%; Score 88.5; DB 2; Length 212;

; Best Local Similarity 27.4%; Pred. No. 0.0036; Matches 32; Conservatve 23; Mismatches 41; Indels 21; Gaps 6;

; APPLICANT: LIGASLUSTI-GPONVLUVKQGK--REGLIAVLLVLCLISDVLFIACTGLGUDLNSAA 67

; APPLICANT: LUGSAITIVLVLGVGKQGK--REGLIAVLLVLCLISDVLFIACTGLGUDLNSAA 72

; APPLICANT: VFLDIACTGLGVUDLNSAAPIVLDIMRGVIAVLLWFAVMAAK 91

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 109

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 128

RESULT 13

US-09-489-039A-9608

; Sequence 9608; Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Bretton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2109-200401

; CURRENT APPLICATION NUMBER: US/09/489, 039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR FILING DATE: 1999-01-29

; SEQ ID NO 9608

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

; US-09-489-039A-9608

; Query Match 14.2%; Score 88; DB 2; Length 211;

; Best Local Similarity 32.1%; Pred. No. 0.0041; Matches 25; Conservatve 13; Mismatches 36; Indels 4; Gaps 2;

; APPLICANT: LILSISIGPONVLUVKQGK--KREGLAVLLVLCLISDVLFIACTGLGUDLNSAAPIVLDI 73

; APPLICANT: LUTPGPGRMMYUTSRSRICQKGKAGFISLAGVA-VGFFFYMLCAAFGITALVFAVPAVYDA 76

; APPLICANT: MRWGGIAVLLWFAVMAAK 91

; APPLICANT: LRLCGVAVYLWLAQAIK 94

; SEQ ID NO 12661

; LENGTH: 205

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

; US-09-489-039A-12661

; Query Match 14.0%; Score 86.5; DB 2; Length 205;

; Best Local Similarity 29.4%; Pred. No. 0.0062; Matches 30; Conservatve 14; Mismatches 31; Indels 27; Gaps 5;

; APPLICANT: IMRIFITGLLGLASLUSIGPONVLUVKQGK--REGLIAVLLVLCLISDVLFIACTGLGUDLNSAA 49

; APPLICANT: LISAFLYVLTITA--LTPGNNILALSIVSHGLRSRLVLAGHMSVGFITMLIC--- 66

; APPLICANT: LUGSAITIVLVLGVGKQGK--REGLIAVLLVLCLISDVLFIACTGLGUDLNSAA 72

; APPLICANT: VFLDIACTGLGVUDLNSAAPIVLDIMRGVIAVLLWFAVMAAK 91

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 101

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 109

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 128

; APPLICANT: VFLDIACTGLGVUDLNSAAPIVLDIMRGVIAVLLWFAVMAAK 91

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 109

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 128

; APPLICANT: VFLDIACTGLGVUDLNSAAPIVLDIMRGVIAVLLWFAVMAAK 91

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 101

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 109

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 128

; APPLICANT: VFLDIACTGLGVUDLNSAAPIVLDIMRGVIAVLLWFAVMAAK 91

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 101

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 109

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 128

; APPLICANT: VFLDIACTGLGVUDLNSAAPIVLDIMRGVIAVLLWFAVMAAK 91

; APPLICANT: PILFNFIVYVLGKFVLLVIGSKLIVATLGKNSAA-KSPQYQIAFKRKLILSNTP 101

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*  
TITLE OF INVENTION: *AERUGINOSA* FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196\_136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIORITY APPLICATION NUMBER: US 60/074,788  
PRIORITY FILING DATE: 1998-02-18  
PRIORITY APPLICATION NUMBER: US 60/094,190  
PRIORITY FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 18746  
LENGTH: 206  
TYPE: PRT  
ORGANISM: *Pseudomonas aeruginosa*  
US-09-252-991A-18746

Query Match 13.9%; Score 86; DB 2; Length 206;  
Best Local Similarity 27.0%; Pred. No. 0.0072; Gaps 6;  
Matches 34; Conservative 17; Mismatches 51; Indels 24;  
Matches 34; Conservative 17; Mismatches 51; Indels 24; Gaps 6;  
Qy 4 MEFITGILGLGASILLSTGPPQNLVVIKOGIKRKGGLIA---VILVCHISDVFLPIAGTLG 59  
Db 10 MSLVLPFLFAVAVASITPGPTNLVLSNS-QRHGLAAAWPIVLGACHAVAILLILG-LG 67  
Qy 60 VILSLNAPIVIDIMRW--GSIAYLWFAVNAAKDAMTNKVEARQPIEEETPTVDDTP 116  
Db 68 IGEELLRRHPLQGLANLWLGVGWLISYLAWSLFRSAGG-----IDGABP---PRR 112  
Qy 117 LGVFGG 122  
Db 113 LGVLGG 118

Search completed: July 19, 2006, 00:32:11  
Job time : 52 secs

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November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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OM protein - protein search, using sw model

Run on: July 19, 2006, 00:43:22 ; Search time 28 Seconds  
 (without alignments)  
 255.388 Million cell updates/sec

Title: US-10-716-470-10  
 perfect score: 620  
 Sequence: 1 MVVIMIFITGULLGASSLLS..... ETEPTVPPDDTPLGVFGGGH 124

Scoring table: BLASTMS2  
 Gapext 10.0 , Gapext 0.5

Searched: 208217 seqs, 5768156 residues

Total number of hits satisfying chosen parameters: 208217

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications AA New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US09\_NEW\_PUB.pep:\*
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US06\_NEW\_PUB.pep:\*
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US07\_NEW\_PUB.pep:\*
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US08\_NEW\_PUB.pep:\*
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/PC1\_NEW\_PUB.pep:\*
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US10\_NEW\_PUB.pep:\*
 7: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US11\_NEW\_PUB.pep:\*
 8: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	101.5	16.4	205	US-10-471-571A-2892
2	91	14.7	226	Sequence 2892, Ap
3	91	14.7	250	Sequence 7128, Ap
4	89.5	14.4	452	Sequence 7127, Ap
5	80	12.9	484	Sequence 7127, Ap
6	7	12.9	7	Sequence 5197, Ap
7	77.5	12.5	195	Sequence 5196, Ap
8	75.5	12.2	597	Sequence 2, Appl
9	73	11.8	223	Sequence 5385, A
10	73	11.8	594	Db
11	72.5	11.7	432	Sequence 6, IHGFLILAGLILPLGAQNFVFNQGANQPKYRIVLPDIAITAGLSDSLIIAVGVSI 64
12	71	11.5	272	QV
13	70.5	11.4	338	65 NAPIVDIDMRWGGIVLWFA 86
14	70	11.3	847	Db
15	69	11.1	271	66 NSLPVQQLIIVGLFIDMYA 87
16	69	11.1	271	RESULT 2
17	69	11.1	294	US-11-056-355B-7128
18	69	11.1	296	US-11-056-355B-47597
19	69	11.1	357	US-11-056-355B-47596
20	67	10.8	255	US-11-056-355B-100153
21	67	10.8	271	Sequence 106151, Application US/11056355B
22	67	10.8	256	Sequence 47598, A
23	67	10.8	264	Sequence 47997, A
24	67	10.8	264	Sequence 47596, A
25	67	10.8	361	Sequence 47596, A

OTHER INFORMATION: conserved hypothetical

US-10-471-571A-2892

Query Match 16.4%; Score 101.5; DB 6; Length 205;  
 Best Local Similarity 28.0%; Pred. No. 0.0013; Gaps 1;  
 Matches 23; Conservative 20; Mismatches 36; Indices 3; Gaps 1;

QV

8 IIGLIGLGLASSLISIGPQNLVTKQGI---KRBGLIATLVLVCLISDYLFLIAGTGLGVDDLS 64

6 IHGFLILAGLILPLGAQNFVFNQGANQPKYRIVLPDIAITAGLSDSLIIAVGVSI 65

QV

65 NAPIVDIDMRWGGIVLWFA 86

66 NSLPVQQLIIVGLFIDMYA 87

GENERAL INFORMATION:  
 APPLICANT: Brover, Vyacheslav  
 APPLICANT: Alexandrov, Nikolai  
 TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
 FILE REFERENCE: 2750-1590pub2  
 CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2005-02-14  
 PRIORITY APPLICATION NUMBER: 60/544,190  
 PRIOR FILING DATE: 2004-02-13  
 NUMBER OF SEQ ID NOS: 119966  
 SEQ ID NO: 7128  
 LENGTH: 226  
 TYPE: prt  
 ORGANISM: Zea mays subsp. mays  
 FEATURE:  
 NAME/KEY: peptide  
 LOCATION: (1)..(226)  
 OTHER INFORMATION: Ceres Seq. ID no. 12357352  
 ; US-11-056-355B-7128  
 Query Match 14.7%; Score 91; DB 7; Length 226;  
 Best Local Similarity 23.8%; Pred. No. 0.02; Indels 14; Gaps 5;  
 Matches 25; Conservative 26; Mismatches 40; Indels 14; Gaps 5;  
 QY 3 IMBIFITRGLLGLASLUSLISIGPQNLVIKOGIK--REGIATLVLVCLISDVFLIFTAGTG 59  
 DB 105 IMPLAIGLILIFMFFLLIATANAIIVSALMSLAAGGELAIFACLVA-VVI--GAVG 159  
 QY 60 VDILSNAPIVLDIM----RNGGIAVYLWFAVNAKAQMTNQY 98  
 DB 160 VAIKFAISIVISSVGVMITTGWGFWMWFTARKSMQDITKHSI 204  
 ; RESULT 3  
 US-11-056-355B-7127  
 Sequence 7127, Application US/11056355B  
 Publication No. US20060150283A1  
 GENERAL INFORMATION:  
 APPLICANT: Brover, Vyacheslav  
 INVENTOR: Alexandrov, Nickolai  
 TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
 FILE REFERENCE: 2750-1590PUS2  
 CURRENT APPLICATION NUMBER: US/11/056,355B  
 PRIOR APPLICATION NUMBER: 60/544,190  
 PRIOR FILING DATE: 2004-02-13  
 NUMBER OF SEQ ID NOS: 119966  
 SEQ ID NO 7127  
 LENGTH: 250  
 TYPE: prt  
 ORGANISM: Zea mays subsp. mays  
 FEATURE:  
 NAME/KEY: peptide  
 LOCATION: (1)..(250)  
 OTHER INFORMATION: Ceres Seq. ID no. 12357351  
 ; US-11-056-355B-7127  
 Query Match 14.7%; Score 91; DB 7; Length 250;  
 Best Local Similarity 23.8%; Pred. No. 0.022; Indels 14; Gaps 5;  
 Matches 25; Conservative 26; Mismatches 40; Indels 14; Gaps 5;  
 QY 3 IMBIFITRGLLGLASLUSLISIGPQNLVIKOGIK--REGIATLVLVCLISDVFLIFTAGTG 59  
 DB 129 IMPLAIGLILIFMFFLLIATANAIIVSALMSLAAGGELAIFACLVA-VVI--GAVG 183  
 QY 60 VDILSNAPIVLDIM----RNGGIAVYLWFAVNAKAQMTNQY 98  
 DB 184 VAIKFAISIVISSVGVMITTGWGFWMWFTARKSMQDITKHSI 228  
 ; RESULT 4  
 US-11-199-489A-72  
 Sequence 72, Application US/11199489A  
 Publication No. US20060134745A1  
 GENERAL INFORMATION:  
 APPLICANT: Klaenhammer, Todd R.  
 APPLICANT: Russell, William M.  
 APPLICANT: Altermann, Eric  
 ; US-11-199-489A-72  
 Query Match 14.4%; Score 89.5; DB 7; Length 452;  
 Best Local Similarity 22.4%; Pred. No. 0.065; Indels 53; Gaps 6;  
 Matches 35; Conservative 29; Mismatches 39; Indels 53; Gaps 6;  
 QY 7 PITGLLIGASLLI-----SIGPQNLVIKQ 31  
 DB 108 FVTGLLITAILIFENPILHILGAKATYQDADFYRIISTGAAPIVPSIIPON-LIRTE 166  
 QY 32 GIKREGIA---VLIVLCLISDVFLFTI--AGTGIVDILSNAPIVLDIMRNGGIAVYLW 85  
 DB 167 GIAQOMIAITMTGTTAILDPFLFVFKMGSAGIVGIANIOTGYLVTDI-----ILY 218  
 QY 86 AVMAAKDAMTIVKVEAPQIETEPTEPTVPPDTLGVFG 121  
 DB 219 YVLCRTEYIKRKLKYK---SGKTRKDIVAGIPG 251  
 ; RESULT 5  
 US-11-056-355B-5157  
 Sequence 5157, Application US/11056355B  
 Publication No. US20060150283A1  
 GENERAL INFORMATION:  
 APPLICANT: Brover, Vyacheslav  
 INVENTOR: Alexandrov, Nickolai  
 TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
 FILE REFERENCE: 2750-1590PUS2  
 CURRENT APPLICATION NUMBER: US/11/056,355B  
 PRIOR APPLICATION NUMBER: 60/544,190  
 PRIOR FILING DATE: 2004-02-13  
 NUMBER OF SEQ ID NOS: 119966  
 SEQ ID NO 5157  
 LENGTH: 452  
 TYPE: prt  
 ORGANISM: Zea mays subsp. mays  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: (1)..(452)  
 OTHER INFORMATION: Ceres Seq. ID no. 12409681  
 ; US-11-056-355B-5157  
 Query Match 12.9%; Score 80; DB 7; Length 452;  
 Best Local Similarity 27.5%; Pred. No. 0.07; Indels 28; Gaps 6;  
 Matches 33; Conservative 19; Mismatches 40; Indels 28; Gaps 6;  
 QY 14 GASLLISIGPQNLVIKOGIK--REGIATLVL---LVCLISDVFLP---IAGTGVLD 62  
 DB 47 GSSDALQVTERILAVRNACEAPERLALLAARLVEDVACIVADLTLIDVARGVPT 106  
 QY 63 LSNAPIVLDIMRNGGIAVYLWFAVNA---KDAWTNQYEAPOIETEPTVDDTP 116  
 DB 107 L-----VRLTOSAACLRLMFAAPALCDKGYQPAQESOLEAP--VTELPYVURDLP 155  
 ; RESULT 6  
 US-11-056-355B-5156

Sequence 5155, Application US/11056355B  
 Publication No. US20060150283A1

GENERAL INFORMATION:  
 APPLICANT: Bover, Vyacheslav  
 APPLICANT: Alexandrov, Nickolai  
 TITLE OF INVENTION: Polypeptides Encoded Thereby  
 FILE REFERENCE: 2750-1590PUS2  
 CURRENT APPLICATION NUMBER: US/11/056,355B  
 CURRENT FILING DATE: 2005-02-14  
 PRIOR APPLICATION NUMBER: 60/544,190  
 PRIOR FILING DATE: 2004-02-13  
 NUMBER OF SEQ ID NOS: 119966  
 SEQ ID NO 5156  
 LENGTH: 484  
 TYPE: PRT  
 ORGANISM: Zea mays subsp. maya  
 FEATURE:  
 NAME/KEY: peptide  
 LOCATION: (11..(484)  
 OTHER INFORMATION: Ceres Seq. ID no. 12409680

US-11-056-355B-5156

Query Match 12.9%; Score 80; DB 7; Length 484;  
 Best Local Similarity 27.5%; Pred. No. 0.76; Mismatches 40; Indels 28; Gaps 6;  
 Matches 33; Conservative 19; Mismatches 40; Indels 28; Gaps 6;

Qy 14 GASLLISIGPQNVLVIKOGIK--REGIILVU--LVLCLISDVFLP---IAIGLGLD 62  
 Db 79 GSDALQDVTLVTLAVNRAACEAPFRERLALLRREDVACLVADAHLLTDVARGAPT 138

Qy 63 LSNAAPIVLDIMRWGGIAYLLWFAVMAA---KDAAMTNKVAPQIETEETPTVDPDTP 116  
 Db 139 L-----VURTGSAACLRMFAAFPAICDKQYQPAQESQLEAP--VTELPPYVRDLP 187

RESULT 7

US-11-351-137A-2

Sequence 2, Application US/11351137A  
 Publication No. US20060148041A1

GENERAL INFORMATION:  
 APPLICANT: MAIER, THOMAS  
 TITLE OF INVENTION: METHOD FOR FERMENTATIVE PRODUCTION OF AMINO ACIDS AND AMINO ACID DERIVATIVES OF THE PHOSPHOGLYCERATE FAMILY  
 FILE REFERENCE: MAIER, T-2  
 CURRENT APPLICATION NUMBER: US/11/351,137A  
 CURRENT FILING DATE: 2006-02-09  
 PRIOR APPLICATION NUMBER: GERMAN NO. 102 32 930.3  
 PRIOR FILING DATE: 2003-07-19  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 2  
 LENGTH: 195  
 TYPE: PRT  
 ORGANISM: Escherichia coli

US-11-351-137A-2

Query Match 12.5%; Score 77.5; DB 7; Length 195;  
 Best Local Similarity 23.4%; Pred. No. 0.48; Mismatches 37; Indels 43; Gaps 5;  
 Matches 29; Conservative 15; Mismatches 37; Indels 43; Gaps 5;

Qy 3 IMEIFITGLLIGASLLISIGPQNVLVI--KOGIKRPE--GLIAVLVLVCLSD 49  
 Db 5 LLSAFWVYTLTAA--MTPGPNNTLASSATSHGFRQSTRVLAGMSLGLFLMLCADIS 61

Qy 50 VFLFLAGTLGLWDLNSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAAMTNKVAPQIETE 109  
 Db 62 FSLAVIDPAAVHLL-----WAGAYIVLWAKIA-----TSP 94

RESULT 8

US-10-449-902-53836

Query Match 12.2%; Score 75.5; DB 6; Length 597;  
 Best Local Similarity 20.8%; Pred. No. 3; Mismatches 53; Indels 39; Gaps 4;  
 Matches 30; Conservative 22; Mismatches 53; Indels 39; Gaps 4;

Qy 12 LIGASLLISIGPQNVLVIKOGIKREGIILAVLVLCLISDVFLIAGTIVGVLDSNAAPIVL 71  
 Db 197 VLGSAMVYSSAVLQVGLVQGARG---VAVDRVDEYDASEFLAALAVAVVLAAGSVT 253

Qy 72 DINRWGGIAYLLWFAVMAAKDAANTN-----KVEAPQIETE 108  
 Db 254 ---WGAIAFTSLVWVTVVAVAPTHGAPSKHGAEDHTADAFSELCNVAETKPYQDQE 309

US-10-449-902-53836

Query Match 12.2%; Score 75.5; DB 6; Length 597;  
 Best Local Similarity 20.8%; Pred. No. 3; Mismatches 53; Indels 39; Gaps 4;  
 Matches 30; Conservative 22; Mismatches 53; Indels 39; Gaps 4;

Qy 12 LIGASLLISIGPQNVLVIKOGIKREGIILAVLVLCLISDVFLIAGTIVGVLDSNAAPIVL 71  
 Db 197 VLGSAMVYSSAVLQVGLVQGARG---VAVDRVDEYDASEFLAALAVAVVLAAGSVT 253

Qy 72 DINRWGGIAYLLWFAVMAAKDAANTN-----KVEAPQIETE 108  
 Db 310 PLIPLDTPAFLSYVPGDGGDGGGG 333

RESULT 9

US-10-449-902-32208

Query Match 12.2%; Score 75.5; DB 6; Length 597;  
 Best Local Similarity 20.8%; Pred. No. 3; Mismatches 53; Indels 39; Gaps 4;  
 Matches 30; Conservative 22; Mismatches 53; Indels 39; Gaps 4;

Qy 12 LIGASLLISIGPQNVLVIKOGIKREGIILAVLVLCLISDVFLIAGTIVGVLDSNAAPIVL 71  
 Db 197 VLGSAMVYSSAVLQVGLVQGARG---VAVDRVDEYDASEFLAALAVAVVLAAGSVT 253

Qy 72 DINRWGGIAYLLWFAVMAAKDAANTN-----KVEAPQIETE 108  
 Db 310 PLIPLDTPAFLSYVPGDGGDGGGG 333

US-10-449-902-32208

Query Match 11.8%; Score 73; DB 6; Length 223;  
 Best Local Similarity 23.5%; Pred. No. 1.7; Mismatches 40; Indels 14; Gaps 5;

Matches 24; Conservative 24; Mismatches 40; Indels 14; Gaps 5;

Qy 6 1PITGLLIGASLLISIGPQNVLVIKOGIK--REGIILAVLVLCLISDVFLIAGTIVGVL 62

RESULT 10  
 US-10-449-902-38726  
 ; Sequence 38726, Application US/10449902  
 ; Publication No. US20060115490A1  
 GENERAL INFORMATION:  
 ; APPLICANT: National Institute of Agrobiological Sciences, Institution.  
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
 ; APPLICANT: The Institute of Physical and Chemical Research.  
 ; APPLICANT: Foundation for Advancement of International Science.  
 ; TITLE OF INVENTION: FULL LENGTH PLANT CDNA AND USIS THEREOF  
 ; FILE REFERENCE: MOA-A0205Y1-US  
 ; CURRENT APPLICATION NUMBER: US/10/449, 902  
 ; CURRENT FILING DATE: 2003-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2002-203269  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2002-383870  
 ; PRIOR FILING DATE: 2002-12-11  
 ; NUMBER OF SEQ ID NOS: 56791  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 38726  
 ; LENGTH: 594  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; US-10-449-902-38726

Query Match 11.8%; Score 73; DB 6; Length 594;  
 Best Local Similarity 29.6%; Pred. No. 5.5; Mismatches 29; Indels 26; Gaps 6;  
 Matches 29; Conservative 14; Mismatches 29; Indels 26; Gaps 6;

Oy 4 MEIFITGLLIGASULLSGPQNLVVIKQIKREGIALLYV-----CLISD-----V 50  
 Db 192 LSIFIVAGSYCLGLPLW--GP---LSBQYGRVRFVIGMLVYTCFNIGCALSKNTGSLV 244

Oy 51 FVFLIAGTGLGVDLISNAPIVLDIMRWG---GAYLLW 84  
 Db 245 FVFLIAGTGLGVDLISNAPIVLDIMRWG---GAYLLW 280

RESULT 11  
 US-10-471-571A-922  
 ; Sequence 822, Application US/10471571A  
 ; Publication No. US20060115490A1  
 GENERAL INFORMATION:  
 ; APPLICANT: CHIRON SPA  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
 ; FILE REFERENCE: P026927MO  
 ; CURRENT APPLICATION NUMBER: US/10/471,571A  
 ; CURRENT FILING DATE: 2003-09-12  
 ; PRIOR APPLICATION NUMBER: GB-0107661.1  
 ; PRIOR FILING DATE: 2001-03-27  
 ; NUMBER OF SEQ ID NOS: 5642  
 ; SOFTWARE: SeqWin99, version 1.03  
 ; SEQ ID NO 822  
 ; LENGTH: 432  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus aureus  
 ; FEATURE: NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (1)..(432)  
 ; OTHER INFORMATION: aseptical pump membrane  
 ; US-10-471-571A-922

Query Match 11.7%; Score 72.5; DB 6; Length 432;  
 Best Local Similarity 31.1%; Pred. No. 4.3; Mismatches 7; Indels 25; Gaps 3;

RESULT 12  
 US-11-056-355B-24250  
 ; Sequence 24250, Application US/11056355B  
 ; Publication No. US20060150283A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Brover, Vyacheslav  
 ; APPLICANT: Alexandrov, Nikolai  
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
 ; FILE REFERENCE: 2750-1590PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/056, 355B  
 ; CURRENT FILING DATE: 2005-02-14  
 ; PRIOR APPLICATION NUMBER: 60/544,190  
 ; PRIOR FILING DATE: 2004-02-13  
 ; NUMBER OF SEQ ID NOS: 119966  
 ; SEQ ID NO 24250  
 ; LENGTH: 272  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: peptide  
 ; LOCATION: (1)..(272)  
 ; OTHER INFORMATION: (1)..(272)  
 ; US-11-056-355B-24250

Query Match 11.5%; Score 71; DB 7; Length 272;  
 Best Local Similarity 28.5%; Pred. No. 3.6; Mismatches 50; Indels 20; Gaps 7;  
 Matches 37; Conservative 23; Mismatches 50; Indels 20; Gaps 7;

Oy 7 FITGL-----LIGASULLSGPQNLVVIKQIKREGIALLYV-----CLISD-----V 60  
 Db 7 FVGL-----LIGASULLSGPQNLVVIKQIKREGIALLYV-----CLISD-----V 62

Oy 61 --DLISNAPIVLDIMRWG---GAYLLW 103  
 Db 63 IGSCFKENLAWSYLLILFGGIVALMIFSFIFLP--FVTK-GAGRVSGRYKEYTDF 113

Oy 114 DTPLGYFGGG 123  
 Db 120 STWLNGFVGG 129

RESULT 13  
 US-10-471-571A-4172  
 ; Sequence 4172, Application US/10471571A  
 ; Publication No. US20060115490A1  
 GENERAL INFORMATION:  
 ; APPLICANT: CHIRON SPA  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
 ; FILE REFERENCE: P026927MO  
 ; CURRENT APPLICATION NUMBER: US/10/471,571A  
 ; CURRENT FILING DATE: 2003-09-12  
 ; PRIOR APPLICATION NUMBER: GB-0107661.1  
 ; PRIOR FILING DATE: 2001-03-27  
 ; NUMBER OF SEQ ID NOS: 5642  
 ; SOFTWARE: SeqWin99, version 1.03  
 ; SEQ ID NO 4172  
 ; LENGTH: 338  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus aureus  
 ; FEATURE: NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (1)..(338)

; OTHER INFORMATION: ferrichrome transport

US-10-471-571A-4172

Query Match 11.4%; Score 70.5; DB 6; Length 338;  
Best Local Similarity 24.5%; Pred. No. 5.3; Mismatches 25; Conservative 22; Mismatches 40; Indels 15; Gaps 3;

Qy 1 MVIMEIPITGLIGASLLISIGPQNLV----IKQGKREGIAV----LLVCL 47  
Db 11 LIALAVFSLFLPGLCTWSITSGEYNIPVERFFKTLIGQDADLILDFRLPRMMITL 70

Qy 48 SDVFLFIAITGLGVDSLIS-AAPVLDIMRWGGIAYLILWFAV 87  
Db 71 AGAALISGAIQVSVTKPPIAEPQILGINAGGGPAIALPIA 112

RESULT 14

Sequence 70, Application US/11174307B

Publication No. US20060143729A1

GENERAL INFORMATION:

APPLICANT: BROVER, Vyacheslav

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY

TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS

FILE REFERENCE: 275-01601PUS2

CURRENT APPLICATION NUMBER: US/11/174, 307B

CURRENT FILING DATE: 2005-06-30

PRIOR APPLICATION NUMBER: 60/583, 671

PRIOR FILING DATE: 2004-06-30

PRIOR APPLICATION NUMBER: 60/583, 781

PRIOR FILING DATE: 2004-06-30

PRIOR APPLICATION NUMBER: 60/583, 651

PRIOR FILING DATE: 2004-06-30

PRIOR SEQ ID NOS: 5544

SEQ ID NO: 70

LENGTH: 847

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: misc\_feature

LOCATION: misc\_feature

FEATURE:

NAME/KEY: peptide

LOCATION: (1)..(271)

FEATURE:

NAME/KEY: protein

LOCATION: (1)..(271)

FEATURE:

NAME/KEY: protein